

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION EFFICIENCY

<130> 24181WO

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 2284

<212> DNA

<213> *Aspergillus niger*

<400> 1

atggcggacg gcaacccaCa tcgggaagat gaggcggccg aggaagaaga ggagattgat	60
gagactgtac gcaaatttac ccatgaactt ggactggaac tctggaactg acaataagat	120
cagagctaca aaccagtc aa agatgcggtc ctcttcgcaa tcgatgtcag cgattccatg	180
ttgacgcctc gcccctcagc agatcctaag aaacacacccc aagaatcacc caccacggca	240
gcgctcaa at gcgcctat ca ctctcatgcaa caacgaatca tatcaa atcc acaagacatg	300
atgggtgttt tgctgttcgg gacccaggcg tccaagttct ttgaagaaga tgaagacagt	360
cggggagacc tgtcctac cc caactgctac ctcttcactg atctggatgt tccttcgget	420
catgagggtca aaggactt cg agcactggta gatgatgaag gagactcaag ggagggttcta	480
tctccagcga aagagcaggt ctctatggca aacgtcctat tttgcgcaa ccagatatc	540
acatccagag cgccaaat tt cctctcccg cgtttgttca tcataaccga caatgacaac	600
ccccatggtg atgataaa ac cctgcggtca gcggcgactg tacgtgctaa ggatctttac	660
gatcttggtg tcaacaatt ga gctgtttccg atctcacgcc ctgagcatga gttcaagaac	720
agcaagttct atgacgta ag ctatcatact ctatagcaaa gtggcagggg tcgatactca	780
ctacagatac aaaggata tt atctacaagt cattgccag cgatccagag gcgcctgcat	840
atctacaatc tgattcaa aa gcggcgactg cgaccgggga cgggatttca ctctcaaca	900
cgcttctgtc cagtatta at tcgagaacgg ttccgcgtcg cactcatttt tcgaacatgc	960
ctttagaact tggcccag ac ttcagaattt cggtatcggg ctatatactc ttacgaaggc	1020
aagcgcccg tagaaact cc ttcactctggc tgaacggcga gaagcctgtg gtcgcgaaag	1080
gagtgacttc ccactccg ca gatgatactg gccggactgt cgagaaatgg gagatcagaa	1140

```

aggcatataa gttcgggtggc gaccaagtaa ccttttcgcc tgatgagcag aaggcgctta 1200
gggatttcgg tgagccagta atccgggtta ttgggttcaa gcctatcact gcgcttccat 1260
tctgggcaaa cgtcaagcac ccatatttta tctatccatc cgaggaagac tatgtaggct 1320
cctcgcgagt attttccgca ttgcatcaga ctcttttgcg ttccaagaag atggcactcg 1380
tctggttcat tgcacgcaag ggtgctggcc ccgttctcgc cgtatgatc gcaggcgaag 1440
aaaagcttga tgagaatggc gtacaaaaat accctcctgg catgtggatt cttccctcc 1500
ccttcgcaga cgatatccgg cagaaccccg aaacaacggt gaatgtcgcc ccggagtcat 1560
tgattgatca gatgcgcgtg atcgtccagc aactgcagct gccgaaggga gtgtacgagc 1620
ctctcaaata cccaatcca tgtaagtcac ttctgtcttg cattgctcgt atacgatgaa 1680
cgagaagctg acagcccggtg atcagccctt caatggcatt accgcctcct acaagctctc 1740
gcattagacg aagatctccc cgaaaaacca gaagaacaaa ccattccgaa ataccgcaa 1800
atcgacaagg taaatccacc acaccaaca cgagaaataa cctccaggc gtccaactta 1860
ctgacaattg caccacagcg cgcgggtgac tacgtattat cctgggcca cgaactcgaa 1920
aagcaatacg ccaaacctc agcagcgcc cctgcacca ccagcaccct cgtgaaacga 1980
ggatcaaaag accgagcaag cgaaaccgag gactccaagc catcgaaaaa gatcaagggt 2040
gaggaagact ctggaagcct agaggaggaa gtccgcaggc atcacaagaa gggaacgcta 2100
tccaaggtaa gccaccacag gctttctaca cgtccctcgtg atggcaaata tgacatcgt 2160
ttaaccggcg gttttctage ttacggtcgc tatccctcaag gacttcttga cttccaatgg 2220
acgctcaaat gccggtaaga aggcggatct tattgagcgg gtagaggagt tcttgagca 2280
gtga 2284

```

<210> 2
 <211> 1947
 <212> DNA
 <213> *Aspergillus niger*

```

<400> 2
atggcggacg gcaaccacac tcgggaagat gaggcggcgg aggaagaaga ggagattgat 60
gagactagct acaaaccagt caaagatgcg gtccctcttcg caatcgatgt cagcgattcc 120
atgttgacgc ctgcgccctc agcagatcct aagaaacaca cccaagaatc acccaccacg 180
gcagcgctca aatgcgccta tcacttcatg caacaacgaa tcatatcaaa tccacaagac 240
atgatgggtg ttttgctgtt cgggaccacg gcgtccaagt tctttgaaga agatgaagac 300

```

agtcgggggag acctgtccta ccccaactgc tacctcttc a ctgatctgga tgttccttcg	360
gctcatgagg tcaaaggact tcgagcactg gtagatgat g aaggagactc aaggagggtt	420
ctatctccag cgaaagagca ggtctctatg gcaaactgc c tattttgcgc caaccagata	480
ttcacatcca gagcgccaaa tttcctctcc cggcgtttg t tcatcataac cgacaatgac	540
aacccccatg gtgatgataa aaccctgcgg tcagcggcg a ctgtacgtgc taaggatctt	600
tacgatcttg gtgtcacaat tgagctgttt ccgatctca c gccttgagca tgagttcaag	660
aacagcaagt tctatgactc attgcccage gatccagagg cgcttgcata tctacaatct	720
gattcaaaag cggcgactgc gaccggggac gggatttca c tcctcaacac gcttctgtcc	780
agtattaatt cgagaacggt tccgcgtcgc actcatttt t cgaacatgcc tttagaactt	840
ggcccagact tcagaatttc ggtatcgggc tatatactc t tacgaaggca agcgcccgt	900
agaaactcct tcatctggct gaacggcgag aagcctgtgg tcgcgaaagg agtgacttcc	960
cactccgcag atgatactgg ccggactgtc gagaaatggg agatcagaaa ggcatataag	1020
ttcgggtggcg accaagtaac cttttcgct gatgagcaga aggcgcttag ggatttcggt	1080
gagccagtaa tccgggttat tgggttcaag cctatcact g cgcttccatt ctgggcaaac	1140
gtcaagcacc catattttat ctatccatcc gaggaagact atgtaggctc ctgcgcagta	1200
ttttccgcac tgcacagac tcttttgcgt tccaagaaga tggcactcgt ctggttcatt	1260
gcacgcaagg gtgctggccc cgttctcgc gctatgatc g caggcgaaga aaagcttgat	1320
gagaatggcg tacaaaaata ccctcctggc atgtggatt c tccccctccc cttegcagac	1380
gatatccggc agaaccgccg aacaacgttg aatgtcgc c cggagtcatt gattgatcag	1440
atgcgcgtga tcgtccagca actgcagctg ccgaaggga g tgtacgagcc tctcaaatac	1500
ccaatocat cccttcaatg gcattaccgc atcctacaag ctctcgcatt agacgaagat	1560
ctccccgaaa aaccagaaga caaaaccatt ccgaaata c gccaaatcga caagcgcgcc	1620
ggtgactacg tattatcctg ggccgacgaa ctcgaaaagc aatacgccaa aacctcagca	1680
gcggcccctc gcccaaccag caccctcgtg aaacgaggat caaaagaccg agcaagcgaa	1740
accgaggact ccaagccatc gaaaaagatc aaggttgagg aagactctgg aagcctagag	1800
gaggaagtcc gcaggcatca caagaaggga acgctatc ca agcttacggt cgctatcctc	1860
aaggacttct tgacttccaa tggacgtc caaatgcggc a agaaggcgga tcttattgag	1920
cgggtagagg agttcttgga gcagtga	1947

<210> 3
<211> 648
<212> PRT
<213> Aspergillus niger

<400> 3

Met Ala Asp Gly Asn Pro His Arg Glu Asp Glu Ala Ala Glu Glu Glu
1 5 10 15

Glu Glu Ile Asp Glu Thr Ser Tyr Lys Pro Val Lys Asp Ala Val Leu
20 25 30

Phe Ala Ile Asp Val Ser Asp Ser Met Leu Thr Pro Arg Pro Ser Ala
35 40 45

Asp Pro Lys Lys His Thr Gln Glu Ser Pro Thr Thr Ala Ala Leu Lys
50 55 60

Cys Ala Tyr His Phe Met Gln Gln Arg Ile Ile Ser Asn Pro Gln Asp
65 70 75 80

Met Met Gly Val Leu Leu Phe Gly Thr Gln Ala Ser Lys Phe Phe Glu
85 90 95

Glu Asp Glu Asp Ser Arg Gly Asp Leu Ser Tyr Pro Asn Cys Tyr Leu
100 105 110

Phe Thr Asp Leu Asp Val Pro Ser Ala His Glu Val Lys Gly Leu Arg
115 120 125

Ala Leu Val Asp Asp Glu Gly Asp Ser Arg Glu Val Leu Ser Pro Ala
130 135 140

Lys Glu Gln Val Ser Met Ala Asn Val Leu Phe Cys Ala Asn Gln Ile
145 150 155 160

Phe Thr Ser Arg Ala Pro Asn Phe Leu Ser Arg Arg Leu Phe Ile Ile
165 170 175

Thr Asp Asn Asp Asn Pro His Gly Asp Asp Lys Thr Leu Arg Ser Ala
180 185 190

Ala Thr Val Arg Ala Lys Asp Leu Tyr Asp Leu Gly Val Thr Ile Glu
195 200 205

Leu Phe Pro Ile Ser Arg Pro Glu His Glu Phe Lys Asn Ser Lys Phe
210 215 220

Tyr Asp Ser Leu Pro Ser Asp Pro Glu Ala Pro Ala Tyr Leu Gln Ser
225 230 235 240

Asp Ser Lys Ala Ala Thr Ala Thr Gly Asp Gly Ile Ser Leu Leu Asn
245 250 255

Thr Leu Leu Ser Ser Ile Asn Ser Arg Thr Val Pro Arg Arg Thr His
260 265 270

Phe Ser Asn Met Pro Leu Glu Leu Gly Pro Asp Phe Arg Ile Ser Val
275 280 285

Ser Gly Tyr Ile Leu Leu Arg Arg Gln Ala Pro Ala Arg Asn Ser Phe
290 295 300

Ile Trp Leu Asn Gly Glu Lys Pro Val Val Ala Lys Gly Val Thr Ser
305 310 315 320

His Ser Ala Asp Asp Thr Gly Arg Thr Val Glu Lys Trp Glu Ile Arg
325 330 335

Lys Ala Tyr Lys Phe Gly Gly Asp Gln Val Thr Phe Ser Pro Asp Glu
340 345 350

Gln Lys Ala Leu Arg Asp Phe Gly Glu Pro Val Ile Arg Val Ile Gly
355 360 365

Phe Lys Pro Ile Thr Ala Leu Pro Phe Trp Ala Asn Val Lys His Pro
370 375 380

Tyr Phe Ile Tyr Pro Ser Glu Glu Asp Tyr Val Gly Ser Ser Arg Val
385 390 395 400

Phe Ser Ala Leu His Gln Thr Leu Leu Arg Ser Lys Lys Met Ala Leu
405 410 415

Val Trp Phe Ile Ala Arg Lys Gly Ala Gly Pro Val Leu Ala Ala Met
420 425 430

Ile Ala Gly Glu Glu Lys Leu Asp Glu Asn Gly Val Gln Lys Tyr Pro
435 440 445

Pro Gly Met Trp Ile Leu Pro Leu Pro Phe Ala Asp Asp Ile Arg Gln
450 455 460

Asn Pro Glu Thr Thr Leu Asn Val Ala Pro Glu Ser Leu Ile Asp Gln
465 470 475 480

Met Arg Val Ile Val Gln Gln Leu Gln Leu Pro Lys Gly Val Tyr Glu
485 490 495

Pro Leu Lys Tyr Pro Asn Pro Ser Leu Gln Trp His Tyr Arg Ile Leu
500 505 510

Gln Ala Leu Ala Leu Asp Glu Asp Leu Pro Glu Lys Pro Glu Asp Lys
515 520 525

Thr Ile Pro Lys Tyr Arg Gln Ile Asp Lys Arg Ala Gly Asp Tyr Val
530 535 540

Leu Ser Trp Ala Asp Glu Leu Glu Lys Gln Tyr Ala Lys Thr Ser Ala
545 550 555 560

Ala Ala Pro Arg Pro Thr Ser Thr Leu Val Lys Arg Gly Ser Lys Asp
565 570 575

Arg Ala Ser Glu Thr Glu Asp Ser Lys Pro Ser Lys Lys Ile Lys Val
580 585 590

Glu Glu Asp Ser Gly Ser Leu Glu Glu Glu Val Arg Arg His His Lys
595 600 605

Lys Gly Thr Leu Ser Lys Leu Thr Val Ala Ile Leu Lys Asp Phe Leu
610 615 620

Thr Ser Asn Gly Arg Ser Asn Ala Gly Lys Lys Ala Asp Leu Ile Glu
625 630 635 640

Arg Val Glu Glu Phe Leu Glu Gln
645

<210> 4
<211> 2651
<212> DNA
<213> *Aspergillus niger*

<400> 4
atggccgata aagaggcaac tgtctacatc gtggactgcg gcaagtccat gggggagcgg 60
cgtcatggtc gcgaagtgac ggatctcgac tgggcgatgc aatatgtttg ggatcgtatt 120
acagggacgg tgagatcctt attcttgaga atcatatcat acatgaaagc ttatgttttg 180
gataggtggc cactggacga aaaatggctt tgatcgggtg tcttgggctc aggacagatg 240
gtgagtgact agcctcccgg gtacagttgg tagttgtagt ttgctggtcg gggctaagtc 300
aggaacgtcc agaaaccgct aatgagttgg aggatgatcc tgattattcg catatctcgg 360
ttttgtctgg gattaaacag tatgattcat ttttgtctgc tgatcctctg gttattcgct 420
gatgaactat aggtttctta tgccggatat ccgggggttg agcgaccgaa taaagcctag 480
caagactaat aaggagatg gtgagttact cttcttgat ggaattggag tgattggggc 540
tgagccgatg aatatagcta tctctgcact tgtgctcgcg attcagatga ttatcactca 600
gtgcaagaaa ctgaagtaca agcgcaggat tgtcctgggt actaatgggc agggcccgat 660
gaaccggat aatcttagtg aaataacgaa gaagattaag gaggataaca ttgaacttat 720
tattctgtta gtgtcaattg atacactgag agaaccgggg tactaacatg ctgcagggga 780
ccagactttg atgatcctga atatgggggtg aaagaggaag ataaagatcc gcgaaaggta 840
tttaacttcg ttccatatgc tctagactaa taataacaat ggctacaggc cgaaaatgaa 900
acactcctgc gtagtcttgc cgaagactgc gaaggagcct atggaaccct agaacaagct 960
gttgccggagc tggaaactcc tegtgtgaaa accacaagga taacagcaag cttcaagggc 1020
catttgcaac taggaaaccc cgcagaatat gatactgcag ttcggatccc tgtggagcgc 1080
tactacagga catacgttgc aaaagctccg tcggctagtc agttcacagt acgtaacgaa 1140
gaggagatgg gaatggccgc ggccgcagcc ggctcgcagg aaggtagttc ccttgtgggt 1200
gttcgaaaca acaggtccta ccaaattgac gatgggacta ctgaagaagg ggtgagggac 1260
gtggatcgag agcaacttgc caagggttat gagtacgggc ggacattggt ccctattagc 1320
gagacggatg agaatatcac caccctagag acatttgccg ctatcgagct tcttgggttt 1380
atacagagcg atcgggtgag ttctaccctc caataactgt tattatgctg ctaagtgggt 1440
tttgccatta gtatgatcga tacatgcaca tgtcgacgac aaacatcacc atcgcgcagc 1500
gcgcgaatga caaggcagca ctgcctcttt cctctttcat acatgcgctg ttcgagctgg 1560

aatcgtagcg tgcgcccgt atggtgctaa aggagaacaa accccctgtc atagtcgtgc 1620
ttgcgccatc aatcgaacct gactacgagt gtctcctcga agcgcagttg ccattcgcag 1680
aagacgtacg aacgtaccgc ttccctccac tcgacagagt cattacagtg tctggtaaag 1740
tggtgacaca gcatcgaaac ctacccaacg acgatctgtt gaatgcgatg gacaaatacg 1800
tgaaaagcat ggagcttacc gatatggacg agaacgggtg agaagaattg gaagtgatct 1860
caacttcact gctgactttg tacaaagtga cccgacggaa tctctcccaa tagacgactc 1920
tttctctcca gtctgcacc ggatcgactc cgcaatccgt caccgtgcc a ttcaccccaa 1980
cgacctatc ccgccccag cctcagtcct aacgaagttc tcccaccctc cggatgacct 2040
cgtcgagaag tccaagaaat acctagacaa gctagtagca gtgtcggacg tcaagaaagg 2100
tcagtccatc tcggccttga gcctcttagg ccccatcat actcacagtg atgaatctag 2160
tcccacaaa aaccaaaggc accaaacgga cccgcgaaac cgagaagcca ctatccggtc 2220
tcgacgtcga tgcccttctc caccaagaga agcgcacgaa gatctcacc aacaacgcaa 2280
ttcccgagtt taagcagacg ctctcgcagg cagagaacat cgagatcatc aaggatgcag 2340
tgaagcagat gagcactatc attgaagacc aaatcaggca tagtcttggc gatgttaatt 2400
atcatcgggt cactgagggg ctaggtgtga tgcgggagga actgatcgat tatgaggaac 2460
ctgctctgta taacgatttc ttgaagcagc tgaaggagaa gttgttgaaa gaggagctcg 2520
gtggggatcg acgggagctg tgggtggctgc taagaaggag taagttgggg ttgattgaac 2580
agagggagtc ggaacactct gaggtgagag aagaggaagc gaaggcgttt atgtctatgg 2640
ctgctaagtg a 2651

<210> 5
<211> 2178
<212> DNA
<213> *Aspergillus niger*

<400> 5
atggccgata aagaggcaac tgtctacatc gtggactgcg gcaagtccat gggggagcgg 60
cgtcatggtc gcaagtgac ggatctcgac tgggcgatgc aatatgtttg ggatcgtatt 120
acagggacgg tggccactgg acgaaaaatg gctttgatcg gtgttcttgg gctcaggaca 180
gatgtttgct ggtcggggct aatgcaggaa cgtccagaaa ccgctaata gttggaggat 240
gatcctgatt attcgcatac ctcggttttg tctgggatta aacagtttct tatgccggat 300
atccgggggt tgagcgaccg aataaagcct agcaagacta ataagggaga tgctatctct 360

gcacttgtgc tcgcgattca gatgattatc actcagtgcg agaaactgaa gtacaagcgc	420
aggattgtcc tggttactaa tgggcagggc ccgatgaacc cggataatct tagtgaaata	480
acgaagaaga ttaaggagga taacattgaa cttattattc tgggaccaga ctttgatgat	540
cctgaatatg gggtgaaaga ggaagataaa gatccgcgaa aggccgaaaa tgaaacactc	600
ctgcgtagtc ttgcgaaga ctgcgaagga gcctatggaa ccctagaaca agctgttgcg	660
gagctggaaa ctctcgtgt gaaaaccaca aggataacag caagcttcaa gggccatttg	720
caactaggaa accccgcaga atatgatact gcagttcgga tccctgtgga gcgctactac	780
aggacatacg ttgcaaaagc tccgtcggct agtcagttca cagtacgtaa cgaagaggag	840
atgggaatgg ccgcggccgc agccggctcg caggaaggta gttcccttgt ggggtgttca	900
aacaacaggt cctaccaaat tgacgatggg actactgaag aaggggtgag ggacgtggat	960
cgagagcaac ttgccaaggg ttatgagtac gggcggacat tggtcctat tagcgagacg	1020
gatgagaata tcaccaccct agagacattt gcggctatcg agcttcttgg gtttatacag	1080
agcgatcggc atgatcgata catgcacatg tcgacgacaa acatcatcat cgcgcagcgc	1140
gcgaatgaca aggcagcact cgctctttcc tctttcatac atgcgctgtt cgagctggaa	1200
tcgtacgctg tcgcccgtat ggtgctaaag gagaacaaac cccctgtcat agtcgtgctt	1260
gcgccatcaa tcgaaccga ctacgagtgt ctctcgaag cgcagttgcc attcgcagaa	1320
gacgtacgaa cgtaccgctt ccctccactc gacagagtca ttacagtgtc tggtaaagtg	1380
gtgacacagc atcgaaacct acccaacgac gatctgttga atgcgatgga caaatacgtg	1440
aaaagcatgg agcttaccga tatggacgag aacggtgacc cgacggaatc tctcccaata	1500
gacgactctt tctctccagt cctgcaccgg atcgactccg caatccgtca ccgtgccatt	1560
catcccaacg accctatccc gccccagcc tcagtcctaa cgaagttctc ccaccctccg	1620
gatgacctcg tcgagaagtc caagaaatac ctagacaagc tagtagcagt gtcggacgtc	1680
aagaaagtcc caccaaaaac caaaggcacc aaacggaccc gcgaaaccga gaagccacta	1740
tccggtctcg acgtcgatgc ccttctccac caagagaagc gcacgaagat ctcaccaac	1800
aacgcaattc ccgagtttaa gcagacgctc tcgcaggcag agaacatcga gatcatcaag	1860
gatgcagtga agcagatgag cactatcatt gaagaccaa tcaggcatag tcttggcgat	1920
gttaattatc atcgggtcac tgaggggcta ggtgtgatgc gggaggaact gatcgattat	1980
gaggaacctg ctctgtataa cgatttcttg aagcagctga aggagaagtt gttgaaagag	2040

gagctcggtg gggatcgacg ggagctgtgg tggctgctaa gaaggagtaa gttgggggtg 2100
 attgaacaga gggagtcgga acactctgag gtgagagaag aggaagcgaa ggcgtttatg 2160
 tctatggctg ctaagtga 2178

<210> 6
 <211> 725
 <212> PRT
 <213> Aspergillus niger

<400> 6

Met Ala Asp Lys Glu Ala Thr Val Tyr Ile Val Asp Cys Gly Lys Ser
 1 5 10 15

Met Gly Glu Arg Arg His Gly Arg Glu Val Thr Asp Leu Asp Trp Ala
 20 25 30

Met Gln Tyr Val Trp Asp Arg Ile Thr Gly Thr Val Ala Thr Gly Arg
 35 40 45

Lys Met Ala Leu Ile Gly Val Leu Gly Leu Arg Thr Asp Val Cys Trp
 50 55 60

Ser Gly Leu Met Gln Glu Arg Pro Glu Thr Ala Asn Glu Leu Glu Asp
 65 70 75 80

Asp Pro Asp Tyr Ser His Ile Ser Val Leu Ser Gly Ile Lys Gln Phe
 85 90 95

Leu Met Pro Asp Ile Arg Gly Leu Ser Asp Arg Ile Lys Pro Ser Lys
 100 105 110

Thr Asn Lys Gly Asp Ala Ile Ser Ala Leu Val Leu Ala Ile Gln Met
 115 120 125

Ile Ile Thr Gln Cys Lys Lys Leu Lys Tyr Lys Arg Arg Ile Val Leu
 130 135 140

Val Thr Asn Gly Gln Gly Pro Met Asn Pro Asp Asn Leu Ser Glu Ile
 145 150 155 160

Thr Lys Lys Ile Lys Glu Asp Asn Ile Glu Leu Ile Ile Leu Gly Pro
 165 170 175

Asp Phe Asp Asp Pro Glu Tyr Gly Val Lys Glu Glu Asp Lys Asp Pro
180 185 190

Arg Lys Ala Glu Asn Glu Thr Leu Leu Arg Ser Leu Ala Glu Asp Cys
195 200 205

Glu Gly Ala Tyr Gly Thr Leu Glu Gln Ala Val Ala Glu Leu Glu Thr
210 215 220

Pro Arg Val Lys Thr Thr Arg Ile Thr Ala Ser Phe Lys Gly His Leu
225 230 235 240

Gln Leu Gly Asn Pro Ala Glu Tyr Asp Thr Ala Val Arg Ile Pro Val
245 250 255

Glu Arg Tyr Tyr Arg Thr Tyr Val Ala Lys Ala Pro Ser Ala Ser Gln
260 265 270

Phe Thr Val Arg Asn Glu Glu Glu Met Gly Met Ala Ala Ala Ala Ala
275 280 285

Gly Ser Gln Glu Gly Ser Ser Leu Val Gly Val Arg Asn Asn Arg Ser
290 295 300

Tyr Gln Ile Asp Asp Gly Thr Thr Glu Glu Gly Val Arg Asp Val Asp
305 310 315 320

Arg Glu Gln Leu Ala Lys Gly Tyr Glu Tyr Gly Arg Thr Leu Val Pro
325 330 335

Ile Ser Glu Thr Asp Glu Asn Ile Thr Thr Leu Glu Thr Phe Ala Ala
340 345 350

Ile Glu Leu Leu Gly Phe Ile Gln Ser Asp Arg Tyr Asp Arg Tyr Met
355 360 365

His Met Ser Thr Thr Asn Ile Ile Ile Ala Gln Arg Ala Asn Asp Lys
370 375 380

Ala Ala Leu Ala Leu Ser Ser Phe Ile His Ala Leu Phe Glu Leu Glu
385 390 395 400

Ser Tyr Ala Val Ala Arg Met Val Leu Lys Glu Asn Lys Pro Pro Val
405 410 415

Ile Val Val Leu Ala Pro Ser Ile Glu Pro Asp Tyr Glu Cys Leu Leu
420 425 430

Glu Ala Gln Leu Pro Phe Ala Glu Asp Val Arg Thr Tyr Arg Phe Pro
435 440 445

Pro Leu Asp Arg Val Ile Thr Val Ser Gly Lys Val Val Thr Gln His
450 455 460

Arg Asn Leu Pro Asn Asp Asp Leu Leu Asn Ala Met Asp Lys Tyr Val
465 470 475 480

Lys Ser Met Glu Leu Thr Asp Met Asp Glu Asn Gly Asp Pro Thr Glu
485 490 495

Ser Leu Pro Ile Asp Asp Ser Phe Ser Pro Val Leu His Arg Ile Asp
500 505 510

Ser Ala Ile Arg His Arg Ala Ile His Pro Asn Asp Pro Ile Pro Pro
515 520 525

Pro Ala Ser Val Leu Thr Lys Phe Ser His Pro Pro Asp Asp Leu Val
530 535 540

Glu Lys Ser Lys Lys Tyr Leu Asp Lys Leu Val Ala Val Ser Asp Val
545 550 555 560

Lys Lys Val Pro Pro Lys Thr Lys Gly Thr Lys Arg Thr Arg Glu Thr
565 570 575

Glu Lys Pro Leu Ser Gly Leu Asp Val Asp Ala Leu Leu His Gln Glu
580 585 590

Lys Arg Thr Lys Ile Ser Pro Asn Asn Ala Ile Pro Glu Phe Lys Gln
595 600 605

Thr Leu Ser Gln Ala Glu Asn Ile Glu Ile Ile Lys Asp Ala Val Lys
610 615 620

Gln Met Ser Thr Ile Ile Glu Asp Gln Ile Arg His Ser Leu Gly Asp

[illegible]

```
<210> 7
<211> 4501
<212> DNA
<213> Aspergillus niger
```

<400> 7						
cagctcattc	agagagctac	ccgtagtaga	acaggaatac	tgggggtatt	gtgagaacgc	60
gaccgcacga	ccgcccttcc	cattgccaaa	gccatcttcc	agcaattgtg	tgtacatttg	120
ttcogtcagc	gggttggcgt	aacggaaggc	aacgtacggc	ttgtgaggcg	cagtctccgg	180
gttgatcttg	tccagcagct	tgcacatttc	cttgcatctg	tattccgacc	attttcttat	240
gggtgagcct	ccgccgatgt	ccgcatactg	cttttgaatc	ttgggtgtgc	gtcgtttcga	300
aataagaggc	ccgaggtaat	gctggaactt	gccaaagagga	atcaaatacg	cgtcggcctt	360
gaatagaagt	agaatgttag	aaacgtagca	accagaatga	cagcttgcca	tagtcggaga	420
cgtacaaaga	gccggctgag	gaaatcctct	acttcgtctg	tcgtcgaggg	ccctcccatg	480
ttcaggaaga	ccatggctgt	agggccctta	gagcctgttg	catcctgggt	aaccggaggc	540
actgttggtg	ccagcccaca	tctttgttct	tgcttgatc	cgaacagggt	gcgagaagcc	600
ggtcgcagca	attgccgggg	cagggtaaac	gggcggcgga	gagccatgac	aggtaattgt	660
actqaattcg	gttgacctag	tcaatggagg	taataagaaa	agaccgttcg	tatcgcgcaa	720

gcagatgaac tattcacgcc gcattaaata ttcaaaagat ggacgagtgg caagaacagg 780
tagtgggtgt atacaacagc gcaaggcctt ctggaagctg aaaagtccag aacggcttga 840
tgacggagca ccgagaccac gaccaactcc gactcccgac agccaatgac cggccagcta 900
gcgtcatcaa ttaccgggcg gacatcacat gatgttcgtg tctccccgcg tctttctgcc 960
caccggtt tg atcgcgtccc tcgcgaccgg atccagtga gatatagata gatctatctc 1020
cggctgcagg cagcagaggc caaacaggca gacacaacag cccacttgt tcttggttac 1080
gattcaagtt gtcttaacct ttatacttcc ctctttcaat ttcgataata tottgaatgc 1140
tttaaacgat tccacaacat tctactatgg cggacggcaa cccacatcgg gaagatgagg 1200
cggccgagga agaagaggag attgatgaga ctgtacgcaa atttaccat gaacttggac 1260
tggaactctg gaactgacaa taagatcaga gctacaaacc agtcaaagat gcggtcctct 1320
tcgcaatcga tgtcagcgat tccatgttga cgctcgccc ctacagcagat cctaagaaac 1380
acaccaaga atcaccacc accggcagcgc tcaaatgcgc ctatcacttc atgcaacaac 1440
gaatcatatc aaatccacaa gacatgatgg gtgttttgct gttcgggacc caggcgtcca 1500
agttctttga agaagatgaa gacagtcggg gagacctgtc ctaccccaac tgctacctct 1560
tcaatgatct ggatgttctt tcggctcatg aggtcaaagg acttcgagca ctggtagatg 1620
atgaaggaga ctcaaggag gttctatctc cagcgaaaga gcaggctctt atggcaaacg 1680
tctattttg cgccaaccag atattcacat ccagagcgcc aaatttcctc tccggcggtt 1740
tgttcatcat aaccgacaat gacaaccccc atggtgatga taaaaccctg cggtcagcgg 1800
cgactgtacg tgctaaggat ctttacgato ttggtgtcac aattgagctg tttccgatct 1860
cacgccctga gcatgagttc aagaacagca agttctatga cgtaagctat catactctat 1920
agcaaagtgg caggggtcga tactcactac agatacaaag gatattatct acaagtcatt 1980
gccagcgat ccagaggcgc ctgcatatct acaatctgat tcaaaagcgg cgactgcgac 2040
cggggacggg atttcactcc tcaacacgct tctgtccagt attaattcga gaacggttcc 2100
gcgtcgcact catttttcga acatgccttt agaacttggc ccagacttca gaatttcggt 2160
atcgggctat atactcttac gaaggcaagc gcccgctaga aactccttca tctggctgaa 2220
cggcgagaag cctgtggtcg cgaaaggagt gacttccac tccgcagatg atactggccg 2280
gactgtcgag aaatgggaga tcagaaaggc atataagttc ggtggcgacc aagtaacctt 2340
ttcgctgat gagcagaagg cgcttaggga tttcggtgag ccagtaatcc gggttattgg 2400
gttcaagcct atcactgcgc ttccattctg ggcaaacgct aagcaccat attttatcta 2460

tccatccgag gaagactatg taggtcctc gcgagtattt tccgcattgc atcagactct 2520
tttgcgttcc aagaagatgg cactcgtctg gttcattgca cgcaaggggtg ctggccccgt 2580
tctcgccgct atgatcgag gccaagaaaa gcttgatgag aatggcgtag aaaaataccc 2640
tcctggcatg tggattcttc cctcccctt cgcagacgat atccggcaga accccgaaac 2700
aacgttgaat gtcgccccgg agtcattgat tgatcagatg cgcgtgatcg tccagcaact 2760
gcagctgccg aaggagtgat acgagcctct caaatacccc aatccatgta agtcacttct 2820
gtcttgcatg gtcgtatac gatgaacgag aagctgacag cccgtgatca gcccttcaat 2880
ggcattaccg catcctacaa gctctcgcat tagacgaaga tctccccgaa aaaccagaag 2940
acaaaaccat tccgaaatac cgccaaatcg acaaggtaaa tccaccacac ccaacacgag 3000
aaataaccct ccaggcgctc aacttactga caattgcacc acagcgcgcc ggtgactacg 3060
tattatcctg ggccgacgaa ctcgaaaagc aatacgccaa aacctcagca gcggccccctc 3120
gcccaaccag caccctcggtg aaacgaggat caaaagaccg agcaagcgaa accgaggact 3180
ccaagccatc gaaaaagatc aagggtgagg aagactctgg aagcctagag gaggaagtcc 3240
gcaggcatca caagaaggga acgctatcca aggtaagcca ccacaggctt tctacacgtc 3300
ctcgtgatgg caaatatgac atcgtattaa ccggcggttt tctagcttac ggtcgctatc 3360
ctcaaggact tcttgacttc caatggacgc tcaaatgccg gtaagaagge ggatcttatt 3420
gagcgggtag aggagttctt ggagcagtga catggcgggg ttggttgatt cgctagtgcg 3480
cttctgttgg tggatgtcgt tatgtggtgt cttatctcgg gttaggcgtt cgtgacctga 3540
ggacatgagc ttgtaattaa tgatgggttg gatgtcgcgg tattegttct tcagcgaaac 3600
gtaatggaca cgtatttttag gcgatgtaca gttataaaaa atcgaattcg ctgggctagc 3660
cggacatgtc aaaacgaaga gcattaggag agacatatca ggtccaagtg ctatctttca 3720
aaccagtcgc ttaagatcac cgaggcattt atctccagaa aattcacggg ttcagcaggt 3780
gcgcgtatcc cgaattcaaa ttaatatggg aacgatcgta aataaccacc cagattcgcc 3840
gtaaacgata gtagtcaggc tttgcgcgcg acagaagggg acgagtatgt caactgagtc 3900
aacttgaacc gagcagtcct tgtaaacaaac gccacgctgt ttgtaatatc cttttagaaa 3960
cgtattgtcg ctggcaatta tccacaaaaa atgagtctaa acgggcgaaa aaagtcaccc 4020
gaatgggaga atatgtggaa agaagaaaga aagagagacc aaagcaagag agcgccgaaa 4080
ggaagctatc gtaatatata caagtagaag ccgtgggtat ttttataaaa agcagaaacg 4140

ttaacggtat gcgtagaatg atcaacattg tccataaact tgacagtagc agacttcttc 4200
gtcgggacag ctgagagtag caaagtgtta gtatttagga cgcattcagc aggtaggggg 4260
ggaggggtgc aaaggcaaca tactatatg attctttgcc gaatatgaca tgccagagaa 4320
attccatgac acggccacta ctggcgatc ccttggtcgt atcgattatc cactggcgga 4380
tcttgatgta gtctctcgt ggtcgtcgt ggacctgctc ccgggacacg gcgaattgcg 4440
cacagcacgc cgcgccaatc tgtttcggca tttgcaggaa cttctggtat ttagcttcgt 4500
c 4501

<210> 8
<211> 4702
<212> DNA
<213> *Aspergillus niger*

<400> 8
cactcaggat tcttatactt tatggggccc aagtatctct gcagtcaggc gaccaaggaa 60
cagcgttgca cgctgctgtg gtgggtggct ttcacggctc agtcaatttg cttctgacag 120
aaaatgcgga ggttgatgca tcatgtacac tcattgggac ccggttggcg gcagtcatgc 180
ctcgtaaagt gaagtcctgc tgtggctggt accatcgaag ctgtgctgag caattaattg 240
cttgggggtgc agatattgat cgcattgatg aacgtctggg gactccaatg gacattgcat 300
acaaggcagg aaacaatgag ggtgtggagc tgttacttga gaatggagca ctggatccca 360
aatccacagc gtatccacta aattcggaca attgaccggg cacgaagtgc ttttctgttt 420
gagatatata tggagcactg aagaaaataa tcagagactt gccgtacttg aaaacttgga 480
gaaatgatcg gatcggtaaa tgtccaattt gccctgggtg tctgggctcg caagaccctt 540
ttaaaataat atagacattc acgcactact cgcagcaaat cttaacaatt tgggcttgtc 600
taagctctgg gagatcacta atttattata gaaccttcaa atgtcgatta gtatgtgaga 660
gttatcttgt caattcagcc tgttagtaca ataaaaccca ctcatagcg ctccgtcata 720
tataaaattg tgcactacac tcacttgcca tatatgatgc gcagacacce atgttagtat 780
ctgcaatgct acttcaattt cgccaacaaa ggacctcca taaagtagct actctgcaat 840
ttaaatcact agacttgat cacaatcat gtaaataaag caatacggag tataagctgc 900
ccactgcatg cccctcttag taagcaccca ctgcatgatg tcatgtgctt tcgcgtcccg 960
cccgctccca atcgggaaat atcacgctc tgctactca gagtgcattt ttctgccttg 1020
agctcgtccc ttttatgtcg agccagctgc ggcacgaat ggatctgatt ccatcgataa 1080

tctcagtcac tcataactgaa aatggccgat aaagaggcaa ctgtctacac cgtggactgc 1140
ggcaagtcca tgggggagcg gcgtcatggt cgcgaagtga cggatctcga ctgggcatg 1200
caatatgttt gggatcgtat tacagggacg gtgagatcct tattcttgag aatcatatca 1260
tacatgaaag cttatgtttt ggatagggtg ccactggacg aaaaatggct ttgatcgggtg 1320
ttcttgggct caggacagat ggtgagtgac tagcctcccg ggtacagttg gtagttgtag 1380
tttgctggtc ggggctaata caggaacgct cagaaaccgc taatgagttg gaggatgac 1440
ctgattatcc gcatactctg gttttgtctg ggattaaaca gtatgattca tttttgtctg 1500
ctgacccctt ggttatctgc tgatgaacta taggtttctt atgccggata tccgggggtt 1560
gagcgaccga ataaagccta gcaagactaa taaggagat ggtgagttac tottcttgta 1620
tggaattgga gtgattgggg ctgagccgat gaatatagct atctctgcac ttgtgctcgc 1680
gattcagatg attatcactc agtgcaagaa actgaagtac aagcgcagga ttgtcctggt 1740
tactaatggg cagggcccga tgaaccgga taatcttagt gaaataacga agaagattaa 1800
ggaggataac attgaactta ttattctggt agtgtcaatt gatacactga gagaaccggg 1860
gtactaacat gctgcagggg accagacttt gatgacccg aatatggggg gaaagaggaa 1920
gataaagatc cgcgaaagggt atttaacttc gttccatag ctctagacta ataataacaa 1980
tggtctacagg ccgaaaatga aacactcctg cgtagtcttg ccgaagactg cgaaggagcc 2040
tatggaaccc tagaacaagc tggtgcggag ctggaaactc ctctgtgtaa aaccacaagg 2100
ataacagcaa gcttcaaggg ccatttgcaa ctaggaaacc ccgcagaata tgatactgca 2160
gttcggatcc ctgtggagcg ctactacagg acatacgttg caaaagctcc gtcggctagt 2220
cagttcacag tacgtaacga agaggagatg ggaatggccg cggccgcagc cggctcgcag 2280
gaaggtagtt cccttggtgg tggtcgaaac aacaggctct accaaattga cgatgggact 2340
actgaagaag ggggtgaggga cgtggatcga gagcaacttg ccaaggggta tgagtacggg 2400
cggacattgg tccctattag cgagacggat gagaatatca ccaccctaga gacatttgcg 2460
gctatcgagc ttcttgggtt tatacagagc gatcgggtga gttctaccct ccaataactg 2520
ttattatgct gctaagtggg ttttgccatt agtatgatc atacatgcac atgtcgacga 2580
caaacatcat catcgcgag cgcgcgaatg acaaggcagc actcgtctt tctctttca 2640
tacatgcgct gttcgagctg gaatcgtag ctgtcgcccg tatgggtgta aaggagaaca 2700
aaccctctgt catagtcgtg cttgcgccat caatcgaacc cgactacgag tgtctcctcg 2760
aagcgcagtt gccattcgca gaagacgtac gaacgtaccg ctccctcca ctcgacagag 2820

tcattacagt gtctggtaaa gtggtgacac agcatcgaaa cctacccaac gacgatctgt 2880
tgaatgcat ggacaaatac gtgaaaagca tggagcttac cgatatggac gagaacgggt 2940
gagaagaatt ggaagtgat c tcaacttcac tgctgacttt gtacaaagt acccgacgga 3000
atctctccca atagacgact ctttctctcc agtcctgcac cggatcgact ccgcaatccg 3060
tcaccgtgcc attcatccca acgaccctat cccgccccca gcctcagtc taacgaagtt 3120
ctcccacct ccggatgacc tcgtcgagaa gtccaagaaa tacctagaca agctagtagc 3180
agtgtcggac gtcaagaaag gtcagtcctat ctccggccttg agcctcttag gccccatca 3240
tactcacagt gatgaatcta gtcccaccaa aaaccaaagg caccaaacgg acccgcgaaa 3300
ccgagaagcc actatccggt ctgcacgtcg atgccttct ccaccaagag aagcgcacga 3360
agatctcacc caacaacgca attcccgagt ttaagcagac gctctcgag gcagagaaca 3420
tcgagatcat caaggatgca gtgaagcaga tgagcactat cattgaagac caaatcaggc 3480
atagtcttg cgatgttaat tatcatcggg tcaactgagg gctaggtgtg atgcgggagg 3540
aactgatcga ttatgaggaa cctgctctgt ataacgattt cttgaagcag ctgaaggaga 3600
agttgttgaa agaggagct c ggtggggatc gacgggagct gtggtggctg ctaagaagga 3660
gtaagttggg gttgattgaa cagagggagt cggaaacact tgaggtgaga gaagaggaag 3720
cgaaggcgtt tatgtctatg gctgctaagt gagcagaccg ttattgatcc ctattagtcc 3780
ccgattaagg actgggcaac agttcgataa tgacaaatga acaagctcca atgctgcatg 3840
actgtgctcg ctagagtaca atattcacga taacctgcg ctaagtaaca aggcttatcc 3900
catgccaaat gtaacacaca taacatataa taccaaatc gatgaacagt acacgggata 3960
tcaatcatga ccatgagtag aaatagacat cgcaagcaac cattatatcc acacactcaa 4020
gaaattctcc caatcctctt cttcccaata tcaatcttcc caccacacct atattcaagt 4080
cagcacaact ttaccatcaa aaagtaagaa caagatggga aaaaagaaca tacctcgtag 4140
catcctcacc cgcacaaatc aacaactcat tctgcacctg caactcattg ttaattgcaa 4200
tccccaaact cttctgcgga ttgacaatcc tcatcaactc atccaccgag acatcctgat 4260
cctccatcat ctgcttctgc aactgcacca cccactatt atccaactcg cgcgtcctct 4320
ccgtctccct ccccaacact ctccccgacg accgaatcgc cttcttgccc ccctgcgtcc 4380
ccatcaacgc ctcttatcc tgaatcgacg ccaccgcaat atcaatccga ctcttcgccc 4440
ccatcgcat caacagatcc tccagtcctat ctttctcctt cctcgcgttg atgagtagat 4500

ccttcggtcg tgcgctctct ccttccccga gcgtgttggt cccactaaca ctccatgccg 4560
tggcggtcgt agctgtattt ctgcgcccga gtttacttcc tgggtcttgac cctgcattat 4620
tttctccccc acctccagaa gaagagttac tcaaattcct caaccctctc tccaaactcg 4680
caatcaatcc cccggcccta ac 4702

<210> 9
<211> 3965
<212> DNA
<213> *Aspergillus niger*

<400> 9
gtttgacgcg tttgcagtggt agaagcttcc agctaccgta gattactgat acaaactcaa 60
tacactatatt ctataacctt actgttcaat acagtacgat caaaatttcc ggaatattaa 120
tgttacgggtt accttccata tgtagactag cgcacttggc attagggttc gaaatacgat 180
caaagagtat tgggggggggt gacagcagta atgactccaa ctgtaaatcg gcttctaggc 240
gcgctccatc taaatgttct ggctgtgggtg tacaggggca taaaattacg cactaccgga 300
atcgatagaa ctactcattt ttat atagaa gtcagaattc atgggtgttt gatcatttta 360
aatttttata tggcggtgtg tgggcaactc gcttgccggg gcaactcgt taccgattac 420
gttagggctg atattttacgt aaaaatcgct aagggtatgca agaccctaat actaaaacct 480
cggagtcacac agcatccaag cccaagtcct tcacggagaa accccagcgt ccacatcacg 540
agcgaaggac cacctctagg catcggacgc accatccaat tagaagcagc aaagcgaaac 600
agcccaagaa aaaggtcggc ccgtcggcct tttctgcaac gctgatcacg ggcagcgatc 660
caaccaacac cctccagagt gactaggggc ggaaatttat cgggattaat ttccactcaa 720
ccacaaatca cagtcgtccc cggatattgt ctgcagaatg caatttaaac tcttctgcca 780
atcgcttgga tccccgccc ctggccgtag agcttaaagt atgtcccttg tcgatgcgat 840
gtatcacacac atataaatac tagcaaggga tgccatgctt ggaggatagc aaccgacaac 900
atcacatcaa gctctccctt ctctgaacaa taaacccac agaaggcatt tatgatggtc 960
gcgtgggtgt ctctatttct gtacggcctt caggctcggg cacctgcttt ggctgcaacg 1020
cctgcccact ggcatcgca atccatttat ttccctctca cggatcgatt tgcaaggacg 1080
gatgggtcga cgactgcgac ttgt aatact gcggatcagg tgtgttgta cctactagct 1140
ttcagaaaga ggaatgtaa ctga cttgat atagaaatc tgtggtggaa catggcaggg 1200
catcatcgac aaggtaaatt gcccttttat caaaaaaaaa agaaggaaaa gcagaagaaa 1260
aataaaataa aaagaactct agtcctaacc atcacatagt tggactatat ccagggaatg 1320
ggcttcacag ccactctgat cacc cccgtt acagcccagc tgcccagac caccgcatat 1380
ggagatgcct accatggcta ctggcagcag gatattgtaag tcgatttctt taaatatcta 1440
cctgtcatct ttacatcaa tatgaactaa cttgatgggt ttagatactc totgaacgaa 1500
aactacggca ctgcagatga cttgaaggcg ctctcttcgg cccttcatga gagggggatg 1560
tatcttatgg tcgatgtgggt tgc t aacct atgggttcgt gtcctttgca actgacttcg 1620
cggatatgggt tcatttcagt actgacaatg agtaatatca gggctatgat ggagcgggta 1680
gctcagtcga ttacagtgtg tttaaacctg tcagttccca agactacttc caccggttct 1740
gtttcattca aaactatgaa gatcagactc aggttgagga ttgctggcta ggagataaca 1800
ctgtctcctt gcctgatctc gataccacca aggatgtgggt caagaatgaa tggtagcact 1860
gggtgggac attgggtatcg aactactcca gtaagatatt totccctcat tctacaactt 1920
ggctgatoga tgatacttac gaaatcagtt gacggcctcc gtatcgacac agtaaaacac 1980
gtccagaagg acttctggcc cgggtacaac aaagccgcag gcgtgtactg tatcggcgag 2040
gtgctcgacg gtgatccggc ctacacttgt ccctaccaga acgtcatgga cggcgtactg 2100
aactatccca tgtatgggtc ctccaacctat gagccttctt gcaagtctca totcctaacg 2160
aaacggctaa aaccagttac tatccactcc tcaacgcctt caagtcaacc tccggcagca 2220
tggacgacct ctacaacatg atcaacaccg tcaaatccga ctgtccagac tcaacactcc 2280
tgggcacatt cgtcgagaac cacgacaacc cacgggttcg ttcgtaagtc ttccctttta 2340
ttttccgttc ccaatttcca cacagaacct cacctaaca gagcaaagt acaccaacga 2400
catagccctc gccagaacg tcgcagcatt catcatctc aacgacggaa tccccatcat 2460
ctacgccggc caagaacagc actacgccgg cggaaacgac cccgcgaacc gcgaagcaac 2520

```

ctggctctcg ggcctacccga ccgacagcga gctgtacaag ttaattgcct ccgcgaacgc 2580
aatccggaac tatgccatta gcaaagatac aggattcgtg acctacaagg taagcacaac 2640
ctctaagcat accctaattgg cctatcttca gagtatctga cacaagagac taatcactgg 2700
caatacagaa ctggcccac c tacaagacg acacaacgat cgccatgccc aagggcacag 2760
atgggtcgca gatcgtgact atcttgtcca acaaggggtgc ttccgggtgat tcgtataccc 2820
tctccttgag tgggtgcgggt tacacagccg gccagcaatt gacggagggtc attggctgca 2880
cgaccgtgac ggttggttcg gatggaaatg tgcctgttcc tatggcagggt gggctaccta 2940
gggtattgta tccgactgag aagttggcag gtagcaagat ctgtagtagc tcgtgaagggt 3000
tggagagtat atgatggtac tgctattcaa tctggcattg gacagtgagt ttgagtttga 3060
tgtacataac caaggttgtg tctgtataat atatacatgt aagatacatg agcttcgggtg 3120
atataatata gaagtaccat acagtaccgc gttatgaaaa cacattaatc cggatccttt 3180
cctataatag actagcgtgc ttggcattag ggttcgaaaa acaatcgaag agtataagggt 3240
gatgacagca gtaacgactc caactgtagc ccacatcttg agttcggcaa ctactgttgg 3300
cacgtgacct tgtgccttgt ggtagctcct taactttgtc atcattcgaa gaattttcgt 3360
cccttccocag gtaccatcca aaagacaagc atccgtcgct tcaactctgag atcagatgag 3420
agtaatatgt ttgactgcgt ttgtgatgcg ggtgatgtcc tctgcgatcg gccgcaagct 3480
gtttagtttg ccccggtatc tctgtgcgca cggttgtcc cogaattttc ttagctagtg 3540
taatcacgct attcagaaaag gcttccaaga attaggccgg tagttcggcg cgtttggtgt 3600
cgtcaagctc cagcagtgcg ggggcctcgg ctatgatatg gttagaatgc tcgggggtggg 3660
tcacggcagg acacccgaca ctgcaacgtc taccacattt gagcgttatt ggcagacttg 3720
cggcgagata acgaccgcta gcttgtatca accaaatcca actgaaatta ttgctttgcc 3780
atcccaacag tggatttcgg aggagggagg ggggaagata tacgatgaac ggaagactgg 3840
acaagatacg ttacataaag cagtactact tgtttcaaac tgtgtacaca ccagggctct 3900
cgcttcagcg gagagtgtcg aaagattcag taaaacatcg ccaggggtga tggaaagggg 3960
ttaag 3965

```

<210> 10

<211> 1497

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1) .. (1497)

<400> 10

```

atg gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca 48
Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
1 5 10 15
cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat 96
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
20 25 30
ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg 144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
35 40 45
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc 192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
50 55 60
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc 240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65 70 75 80
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga 288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
85 90 95
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa 336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu

```

aac	tac	ggc	act	gca	gat	gac	ttg	aag	gcg	ctc	tct	tcg	gcc	ctt	cat	384
Asn	Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His	
		115					120					125				
gag	agg	ggg	atg	tat	ctt	atg	gtc	gat	gtg	gtt	gct	aac	cat	atg	ggc	432
Glu	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	
	130						135				140					
tat	gat	gga	gcg	ggt	agc	tca	gtc	gat	tac	agt	gtg	ttt	aaa	ccg	ttc	480
Tyr	Asp	Gly	Ala	Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	
145					150					155					160	
agt	tcc	caa	gac	tac	ttc	cac	ccg	ttc	tgt	ttc	att	caa	aac	tat	gaa	528
Ser	Ser	Gln	Asp	Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	
			165				170				175					
gat	cag	act	cag	gtt	gag	gat	tgc	tgg	cta	gga	gat	aac	act	gtc	tcc	576
Asp	Gln	Thr	Gln	Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser	
		180					185				190					
ttg	cct	gat	ctc	gat	acc	acc	aag	gat	gtg	gtc	aag	aat	gaa	tgg	tac	624
Leu	Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	
	195						200				205					
gac	tgg	gtg	gga	tca	ttg	gta	tcg	aac	tac	tcc	att	gac	ggc	ctc	cgt	672
Asp	Trp	Val	Gly	Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	
	210				215					220						
atc	gac	aca	gta	aaa	cac	gtc	cag	aag	gac	ttc	tgg	ccc	ggg	tac	aac	720
Ile	Asp	Thr	Val	Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	
225					230					235					240	
aaa	gcc	gca	ggc	gtg	tac	tgt	atc	ggc	gag	gtg	ctc	gac	ggg	gat	ccg	768
Lys	Ala	Ala	Gly	Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly	Asp	Pro	
		245					250				255					
gcc	tac	act	tgt	ccc	tac	cag	aac	gtc	atg	gac	ggc	gta	ctg	aac	tat	816
Ala	Tyr	Thr	Cys	Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr	
	260						265				270					
ccc	att	tac	tat	cca	ctc	ctc	aac	gcc	ttc	aag	tca	acc	tcc	ggc	agc	864
Pro	Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	
	275						280				285					
atg	gac	gac	ctc	tac	aac	atg	atc	aac	acc	gtc	aaa	tcc	gac	tgt	cca	912
Met	Asp	Asp	Leu	Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro	
	290					295				300						
gac	tca	aca	ctc	ctg	ggc	aca	ttc	gtc	gag	aac	cac	gac	aac	cca	cgg	960
Asp	Ser	Thr	Leu	Leu	Gly	Thr	Phe	Val	Glu	Asn	His	Asp	Asn	Pro	Arg	
305					310					315					320	
ttc	gct	tct	tac	acc	aac	gac	ata	gcc	ctc	gcc	aag	aac	gtc	gca	gca	1008
Phe	Ala	Ser	Tyr	Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala	
			325				330				335					
ttc	atc	atc	ctc	aac	gac	gga	atc	ccc	atc	atc	tac	gcc	ggc	caa	gaa	1056
Phe	Ile	Ile	Leu	Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly	Gln	Glu	
	340						345				350					
cag	cac	tac	gcc	ggc	gga	aac	gac	ccc	gcg	aac	cgc	gaa	gca	acc	tgg	1104
Gln	His	Tyr	Ala	Gly	Gly	Asn	Asp	Pro	Ala	Asn	Arg	Glu	Ala	Thr	Trp	
	355					360					365					
ctc	tcg	ggc	tac	ccg	acc	gac	agc	gag	ctg	tac	aag	tta	att	gcc	tcc	1152
Leu	Ser	Gly	Tyr	Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile	Ala	Ser	
	370					375					380					
gcg	aac	gca	atc	cgg	aac	tat	gcc	att	agc	aaa	gat	aca	gga	ttc	gtg	1200
Ala	Asn	Ala	Ile	Arg	Asn	Tyr	Ala	Ile	Ser	Lys	Asp	Thr	Gly	Phe	Val	
385					390					395					400	
acc	tac	aag	aac	tgg	ccc	atc	tac	aaa	gac	gac	aca	acg	atc	gcc	atg	1248
Thr	Tyr	Lys	Asn	Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile	Ala	Met	

	405	410	415	
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag				1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys				
	420	425	430	
ggg gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac				1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr				
	435	440	445	
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg				1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr				
	450	455	460	
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct				1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro				
	465	470	475	480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt				1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser				
	485	490	495	
agc tcg tga				1497
Ser Ser				

<210> 11
 <211> 498
 <212> PRT
 <213> Aspergillus niger

<400> 11
 Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
 1 5 10 15
 Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
 20 25 30
 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 35 40 45
 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 50 55 60
 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 65 70 75 80
 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 85 90 95
 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 100 105 110
 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 115 120 125
 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 130 135 140
 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 145 150 155 160
 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 165 170 175
 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 180 185 190
 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 195 200 205
 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 210 215 220
 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 225 230 235 240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270
 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 290 295 300
 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335
 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 415
 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
 450 455 460
 Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
 465 470 475 480
 Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
 485 490 495
 Ser Ser

<210> 12

<211> 3697

<212> DNA

<213> *Aspergillus niger*

<400> 12

cttgaataac	gcttcctcaa	tgctgtat	cgaaaagaaa	cgggctttct	ttatccaatc	60
cctgtggtaa	gattgatcgt	caggagatta	tctgcaggaa	acatcatggg	ggggtaacca	120
aggttgtgtc	tgtataatat	atacatgtaa	gatacatgag	cttcgggtgat	ataatacaga	180
agtaccatac	agtaccgcgt	tatgaaaaca	cattaatccg	gaccccttcc	tataatagac	240
tagcgtgctt	ggcattagg	ttcgaaaaac	aatcgaagag	tataaggggga	tgacagcagt	300
aacgactcca	actgtacgcc	tccgggtagt	agaccgagca	gccgagccag	ctcagcgcct	360
aaaacgcctt	atacaattaa	gcagttaaag	aagttagaat	ctacgccttaa	aaagctactt	420
aaaaatcgat	ctcgcagtc	cgattcgcct	atcaaaacca	gtttaaatca	actgattaaa	480
ggtgccgaac	gagctataaa	tgatataaca	atattaaagc	attaattaga	gcaatatcag	540
gccgcgcacg	aaaggcaact	taaaaagcga	aagcgcctcta	ctaaaacagat	tacttttgaa	600
aaaggcacat	cagtatttaa	agcccgaatc	cttattaagc	gccgaaatca	ggcagataaa	660
gccatacagg	cagatagacc	tctacctatt	aaatcggcct	ctaggcgcgc	tccatctaaa	720
tggtctggtc	gtgggtgtaca	ggggcataaa	attacgcact	accggaatcg	atagaactac	780
tcatTTTTat	atagaagtca	gaattcatgg	tgTTTTgatc	atttttaaatt	tttatatggc	840
gggtgggtggg	caactcgctt	gcgcgggcaa	ctcgcttacc	gattacgtta	gggctgatat	900
ttacgtaaaa	atcgtcaagg	gatgcaagac	caaagtagta	aaaccCcgga	gtcaacagca	960

tccaagccca	agtcccttcac	ggagaaaccc	cagcgtccac	atcacgagcg	aaggaccacc	1020
tctaggcatc	ggacgcacca	tccaattaga	agcagcaaag	cgaaacagcc	caagaaaaag	1080
gtcggcccg	cgcccttttc	tgcaacgctg	atcacgggca	gcgatccaac	caacaccctc	1140
cagagtgact	agggggcgaa	atttaaagg	attaatttcc	actcaaccac	aatcacagt	1200
cgtccccggt	attgtcctgc	agaatgcaat	ttaaactctt	ctgcgaatcg	cttggattcc	1260
ccgcccctgg	ccgtagagct	taaagtatgt	cccttgtcga	tgcgatgtat	cacaaatat	1320
aaatactagc	aagggatgcc	atgcttgag	gatagcaacc	gacaacatca	catcaagctc	1380
tcccttctct	gaacaataaa	ccccacagaa	ggcatttatg	atggtcgcgt	ggtggtctct	1440
atttctgtac	ggccttcagg	tcgcggcacc	tgctttggct	gcaacgcctg	cggactggcg	1500
atcgcaatcc	atttatttcc	ttctcacgga	tcgatttgca	aggacggatg	ggtcgacgac	1560
tgcgacttgt	aatactgcgg	atcaggtgtg	ttgttaccta	ctagctttca	gaaagaggaa	1620
tgtaaactga	cttgatatag	aaatactgtg	gtggaacatg	gcagggcatc	atcgacaagg	1680
taaattgccc	ctttatcaaa	aaaaaagaag	gaaaagcaga	agaaaaataa	aataaaaaga	1740
actctagtcc	taaccatcac	atagttggac	tatatccagg	gaatgggctt	cacagccatc	1800
tggatcaccc	ccgttacagc	ccagctgccc	cagaccaccg	catatggaga	tgccaccat	1860
ggctactggc	agcaggatat	gtaagtcat	ttctttaaat	atctacctgt	catcttttac	1920
atcaatatga	actaacttga	tggtttttaga	tactctctga	acgaaaacta	cggcactgca	1980
gatgacttga	agggcgtctc	ttcggccctt	catgagaggg	ggatgtatct	tatggtcgat	2040
gtggttgcta	accatatggg	tcgtggctct	ttgcaactga	cttcgcggat	atgggtcatt	2100
tcagtactga	caatgagtaa	tatcagggct	atgatggagc	gggtagctca	gtcgattaca	2160
gtgtgtttaa	accgttcagt	tccaagact	acttccaccc	gttctgtttc	attcaaaact	2220
atgaagatca	gactcagggt	gaggattgct	ggctaggaga	taacactgtc	tccttgccctg	2280
atctcgatac	caaccaaggat	gtgggtcaaga	atgaatggta	cgactgggtg	ggatcattgg	2340
tatcgaaacta	ctccagtaag	atatttctcc	ctcattctac	aacttggctg	atcgatgata	2400
cttacgaaat	cagttgacgg	cctccgtatc	gacacagtaa	aacacgtcca	gaaggacttc	2460
tggcccggt	acaacaaagc	cgcaggcgtg	tactgtatcg	gcgagggtgt	cgacgggtgat	2520
ccggcctaca	cttgtcccta	ccagaacgtc	atggacggcg	tactgaacta	tcccatgtat	2580
ggttccctcca	accatgagcc	ttcttgcaag	tctcatctcc	taacgaaacg	gctaaaacca	2640
gttactatcc	actcctcaac	gccttcaagt	caacctccgg	cagcatggac	gacctctaca	2700
acatgatcaa	caccgtcaaa	tcgcactgtc	cagactcaac	actcctgggc	acattcgctc	2760
agaaccacga	caacccacgg	ttcgcttctg	aagtcttccc	ttttattttc	cgttcccaat	2820
ttccacacag	aaacccacct	aacaagagca	aagttacacc	aacgacatag	ccctcgccaa	2880
gaacgtcgca	gcattcatca	tcctcaacga	cggaatcccc	atcatctacg	ccggccaaga	2940
acagcactac	gcggcgga	acgacccgc	gaaccgcgaa	gcaacctggc	tctcgggcta	3000
cccgaccgac	agcgagctgt	acaagttaat	tgcctccgcg	aacgcaatcc	ggaactatgc	3060
cattagcaaa	gatacaggat	tcgtgacct	caaggtaagc	acaacctcta	agcataccct	3120
aatggcctat	cttcagagta	tctgacacaa	gagactaatc	actggcaata	cagaaactggc	3180
ccatctacaa	agacgacaca	acgategcca	tgcgcaaggg	cacagatggg	tcgcagatcg	3240
tgactatctt	gtccaacaag	ggtgcttcgg	gtgattcgta	tacctctctc	ttgagtgggtg	3300
cgggttacac	agccggccag	caattgacgg	aggtcattgg	ctgcacgacc	gtgacgggtg	3360
gttcggatgg	aaatgtgcct	gttcctatgg	caggtgggct	acctagggta	ttgtatccga	3420
ctgagaagtt	ggcaggtagc	aagatctgta	gtagctcgtg	aagggtggag	agtatatgat	3480
ggtactgcta	ttcaatctgg	cattggacag	tgagtttgag	tttgatgtac	agttggagtc	3540
gttactgctg	tcacccctt	atactcttcg	attgtttttc	gaacccta	gccaagcacg	3600
ctagtctatt	ataggaaagg	atccggatta	atgtgttttc	ataacgcggg	actgtatggg	3660
acttctgtat	tatatcaccc	aagctcatgt	atcttac			3697

<210> 13

<211> 1497

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1) .. (1497)

<400> 13

atg gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca	48
Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala	
1 5 10 15	
cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat	96
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr	
20 25 30	
ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg	144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala	
35 40 45	
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc	192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly	
50 55 60	
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc	240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile	
65 70 75 80	
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga	288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly	
85 90 95	
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa	336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu	
100 105 110	
aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat	384
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His	
115 120 125	
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc	432
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly	
130 135 140	
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc	480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe	
145 150 155 160	
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa	528
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu	
165 170 175	
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc	576
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser	
180 185 190	
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac	624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr	
195 200 205	
gac tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt	672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg	
210 215 220	
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac	720
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn	
225 230 235 240	
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg	768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro	
245 250 255	
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat	816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr	
260 265 270	
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc	864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser	
275 280 285	
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca	912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro	

290	295	300	
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg			960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg			
305	310	315	320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca			1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala			
	325	330	335
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa			1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu			
	340	345	350
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg			1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp			
	355	360	365
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc			1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser			
	370	375	380
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg			1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val			
	385	390	400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg			1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met			
	405	410	415
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag			1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys			
	420	425	430
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac			1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr			
	435	440	445
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg			1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr			
	450	455	460
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct			1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro			
	465	470	475
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt			1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser			
	485	490	495
agc tcg tga			1497
Ser Ser			

<210> 14

<211> 498

<212> PRT

<213> Aspergillus niger

<400> 14

Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala	
1	5 10 15
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr	
	20 25 30
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala	
	35 40 45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly	
	50 55 60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile	

65					70					75					80
Trp	Ile	Thr	Pro	Val	Thr	Ala	Gln	Leu	Pro	Gln	Thr	Thr	Ala	Tyr	Gly
				85					90					95	
Asp	Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu
			100					105					110		
Asn	Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His
		115					120					125			
Glu	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly
	130					135					140				
Tyr	Asp	Gly	Ala	Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe
145					150				155						160
Ser	Ser	Gln	Asp	Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu
			165					170						175	
Asp	Gln	Thr	Gln	Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser
		180						185					190		
Leu	Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr
	195						200					205			
Asp	Trp	Val	Gly	Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg
	210				215						220				
Ile	Asp	Thr	Val	Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn
225				230					235						240
Lys	Ala	Ala	Gly	Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly	Asp	Pro
			245					250						255	
Ala	Tyr	Thr	Cys	Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr
		260						265					270		
Pro	Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser
	275						280					285			
Met	Asp	Asp	Leu	Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro
	290				295						300				
Asp	Ser	Thr	Leu	Leu	Gly	Thr	Phe	Val	Glu	Asn	His	Asp	Asn	Pro	Arg
305				310					315						320
Phe	Ala	Ser	Tyr	Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala
			325					330						335	
Phe	Ile	Ile	Leu	Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly	Gln	Glu
		340					345						350		
Gln	His	Tyr	Ala	Gly	Gly	Asn	Asp	Pro	Ala	Asn	Arg	Glu	Ala	Thr	Trp
	355					360						365			
Leu	Ser	Gly	Tyr	Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile	Ala	Ser
	370				375						380				
Ala	Asn	Ala	Ile	Arg	Asn	Tyr	Ala	Ile	Ser	Lys	Asp	Thr	Gly	Phe	Val
385				390					395						400
Thr	Tyr	Lys	Asn	Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile	Ala	Met
			405					410						415	
Arg	Lys	Gly	Thr	Asp	Gly	Ser	Gln	Ile	Val	Thr	Ile	Leu	Ser	Asn	Lys
		420					425					430			
Gly	Ala	Ser	Gly	Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala	Gly	Tyr
	435					440						445			
Thr	Ala	Gly	Gln	Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr	Val	Thr
	450				455						460				
Val	Gly	Ser	Asp	Gly	Asn	Val	Pro	Val	Pro	Met	Ala	Gly	Gly	Leu	Pro
465				470					475						480
Arg	Val	Leu	Tyr	Pro	Thr	Glu	Lys	Leu	Ala	Gly	Ser	Lys	Ile	Cys	Ser
			485				490							495	
Ser	Ser														

<211> 3570

<212> DNA

<213> *Aspergillus niger*

<400> 15

ggaaccagta	cggcagctga	tagtatccga	aagctgcaaa	ttgcttc atc	gaggctggca	60
ttcgatagaa	gaaagaatta	tagacaacta	gtcttgcaat	atgacaa ttc	tctttgatta	120
ataaatgaaa	gcacgcgatg	atcagcctaa	tagccgagtg	gcgggca tct	ctggcggcct	180
cccagagcagc	gtggaatgcg	tccaagatcc	cgtccgcggg	tcgtcct tcc	gtcgggaatga	240
tgactggagc	agcagacgat	gtcctgagct	gaatgcgatg	gatattc aca	ttccagggag	300
aattgtcggc	tatttagaac	cctctcggct	taaaagccct	attagac tat	gggtgcgctc	360
aagccactag	ccaggatata	ccgctgaacg	ctccatcacc	ttgcagc tga	agtgcacacat	420
gggacgggct	ttaacttttc	gtagatataa	gtttaattta	tcctctc cac	acccataggg	480
tcgtatgggtg	tcaaccgggtg	tagtctgcag	gatttcatct	cgcttcg cca	agcgaggcgc	540
cctaaccgggc	agcctgcagc	ttaccctggt	aaccccggt	caccacc ccc	cgagcaatcc	600
gtcgcgtcct	ccacgagtc	taacaagggt	cgggcgttgt	ttcttac ccc	cactatcagg	660
cgtattcagt	taacagtcag	tagtcccgtg	tcggagattt	gttggtc tgc	aacaattaaa	720
ggggaccagg	gttaaactct	ggcccccgaa	ctgatccggag	tttcggc caa	tgagagatgt	780
tgtatacccc	cggttcctggc	agatggatta	attgccggct	ccatttg gca	tccatcaagc	840
atcatacggg	attagaaggg	tagttcgtgg	gttgatctgc	cgtgcaa ggt	gctcaaggct	900
ctggagtcct	gctgaacgca	aatatattaag	aatcgtcgtc	agggaca gcg	ttctctggat	960
agtcaagctg	tgcttgggac	gctgttctgt	cgctttgtca	aaacata att	cgcagcgatg	1020
agattatcga	cttcgagctc	cttcctttcc	gtgtctctgc	tggggaa gct	ggccctcggg	1080
ctgtcggctg	cagaatggcg	cactcagtcg	atttacttcc	tattgac gga	tcggttcggg	1140
aggacggaca	attcgacgac	agctacatgc	gatacgggtg	accaagt acg	ttgggtattgc	1200
aggacttcca	tcattcatct	actgacttga	atagatctat	tgtgggtg gca	gttggcaagg	1260
aatcatcaac	catgtttgtg	atcacttcat	actatccgct	gtgcgcgtgt	ctgactttat	1320
ttgctgcagc	tggtattatat	ccagggcatg	ggattcacgg	ccatctg gat	ctcgccctac	1380
actgaacagc	tgccccagga	tactgctgat	gggtgaagctt	accatggata	ttggcagcag	1440
aagatgtatg	cgctcctcct	tcccatatcg	taggcttact	ctcaggc ggc	gactgacttg	1500
acagatacga	cgtgaactcc	aacttcggca	ctgcagatga	cctcaagtcc	ctctcagatg	1560
cgtttcatgc	ccgcgggaatg	tacctcatgg	tggacgtcgt	ccctaaccac	atggtaagtg	1620
ctgcttcagc	atccttatca	gtgaactcca	agtgccaaag	ctaactgtac	cagggctacg	1680
ccggcaacgg	caacgatgta	gactacagcg	tcttcgaccc	cttcgat tcc	tctcctact	1740
tccacccata	ctgcctgatc	acagattggg	acaacttgac	catgggtc caa	gattgtttggg	1800
aggggtgacac	catcgtatct	ctgccagacc	taaacaccac	cgaact gcc	gtgagaacaa	1860
tctgggtatga	ctgggttagcc	gacctgggtat	ccaattatcc	aggtgcgaaat	tccaacccaa	1920
tttaaaataa	ccatataacta	agtgaatatca	ccagtcgacg	gactccgcat	cgacagtgtc	1980
ctcgaagtcg	aaccagactt	cttcccgggc	taccaggaag	cagcaggtgt	ctactgcgtc	2040
ggcgaagtcg	acaacggcaa	ccctgccttc	gactgcccct	accagaa ggt	cctggacggc	2100
gtcctcaact	atccgatgta	ctacccccta	tacattgttc	attagat ctt	cgctaactcc	2160
aaccagctac	tggcaactcc	tctacgcctt	cgaatccctc	agcggcagca	tcagcaacct	2220
ctacaacatg	atcaaatccg	tcgcaagcga	ctgtccgat	ccgacactac	tcggcaactt	2280
catcgaaaac	cacgacaatc	cccgtttcgc	ctcgtatgtc	ccaccccctc	ccctccctac	2340
aatcacactc	actaatacat	ctaacagcta	cacctccgac	tactcgcaag	ccaaaaacgt	2400
cctcagctac	atcttcctct	cggacggcat	ccccatcgtc	tacgcccggc	aagaacagca	2460
ctactccggc	ggcaagggtg	cctacaaccg	cgaagcgacc	tggctttcag	gctaogacac	2520
ctccgcagag	ctgtacacct	ggatagccac	cacgaacggc	atccgcaaac	tagccatctc	2580
agctgactcg	gcctacatta	cctacgcggg	tcgtccttcc	ctcccaacct	ttacccccca	2640
ccctacaaac	atcccacata	ctaacaacat	ttcaataatg	aaatagaatg	atgcattcta	2700
cactgacagc	aacaccatcg	caatgcgcaa	aggcacctca	gggagccaag	tcataaccgt	2760
cctctccaac	aaaggctcct	caggaagcag	ctacacctg	accctcagcg	gaagcggcta	2820
cacatccggc	acgaagctga	tcgaagcgta	cacatgcaca	tccgtgaccg	tggactcgag	2880
cggcgatatt	cccgtgccga	tggcgtcggg	attaccgaga	gttcttctgc	ccgcgtccgt	2940
cgtcgatagc	tcttcgctct	gtggcggggag	cgggaagatta	tacgtcggag	aatccggagt	3000
ggtcgggttac	tgtgacgttg	ccgggtgggga	ccactttcga	gtataagttt	attaagggtg	3060
agtcggatgg	gactgttact	tgggaaagtg	attcgaatcg	ggagtat acg	gtgccggagt	3120

```

gtgggagtg ggagacggtg gttgatactt ggaggtagat gatctgagat ttctaagtgt 3180
gatgaggggtg gttttgggtg atgtagtttg gcctttggta gtgttgggtt gggttgggtt 3240
aataattatg ttattgtttt tgggtgcttgt gaccatggat ttgaagtga aatttgtagg 3300
ggctacggaa gtgtattgtg gacatgtgag taaattcatc tgggtatgta caaagtgggt 3360
tagccagtgg gcttgaagaa aagtctcctg ggtctctggt ttgagtaccc atgttaagat 3420
caagcataaa aacatgaaat attgggaaaa caaagggtat ttaacaactc gtgagcatta 3480
gctcctgggt agaatgcaat cataacagaa agtacagcca gcgctgtgtc ataaagaagt 3540
ccagttggga aacgaaagac tagaatcaaa 3570

```

<210> 16
 <211> 1518
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(1518)

```

<400> 16
atg aga tta tcg act tcg agt ctc ttc ctt tcc gtg tct ctg ctg ggg 48
Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly
1 5 10 15
aag ctg gcc ctc ggg ctg tcg gct gca gaa tgg cgc act cag tcg att 96
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
20 25 30
tac ttc cta ttg acg gat cgg ttc ggt agg acg gac aat tcg acg aca 144
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
35 40 45
gct aca tgc gat acg ggt gac caa atc tat tgt ggt ggc agt tgg caa 192
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
50 55 60
gga atc atc aac cat ctg gat tat atc cag ggc atg gga ttc acg gcc 240
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65 70 75 80
atc tgg atc tcg cct atc act gaa cag ctg ccc cag gat act gct gat 288
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
85 90 95
ggt gaa gct tac cat gga tat tgg cag cag aag ata tac gac gtg aac 336
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
100 105 110
tcc aac ttc ggc act gca gat gac ctc aag tcc ctc tca gat gcg ctt 384
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
115 120 125
cat gcc cgc gga atg tac ctc atg gtg gac gtc gtc cct aac cac atg 432
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
130 135 140
ggc tac gcc ggc aac ggc aac gat gta gac tac agc gtc ttc gac ccc 480
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
145 150 155 160
ttc gat tcc tcc tcc tac ttc cac cca tac tgc ctg atc aca gat tgg 528
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
165 170 175
gac aac ttg acc atg gtc caa gat tgt tgg gag ggt gac acc atc gta 576
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
180 185 190
tct ctg cca gac cta aac acc acc gaa act gcc gtg aga aca atc tgg 624

```


Ser	Leu	Pro	Asp	Leu	Asn	Thr	Thr	Glu	Thr	Ala	Val	Arg	Thr	Ile	Trp	
		195					200					205				
tat	gac	tgg	gta	gcc	gac	ctg	gta	tcc	aat	tat	tca	gtc	gac	gga	ctc	672
Tyr	Asp	Trp	Val	Ala	Asp	Leu	Val	Ser	Asn	Tyr	Ser	Val	Asp	Gly	Leu	
		210					215					220				
cgc	atc	gac	agt	gtc	ctc	gaa	gtc	gaa	cca	gac	ttc	ttc	ccg	ggc	tac	720
Arg	Ile	Asp	Ser	Val	Leu	Glu	Val	Glu	Pro	Asp	Phe	Phe	Pro	Gly	Tyr	
225					230					235					240	
cag	gaa	gca	gca	ggg	gtc	tac	tgc	gtc	ggc	gaa	gtc	gac	aac	ggc	aac	768
Gln	Glu	Ala	Ala	Gly	Val	Tyr	Cys	Val	Gly	Glu	Val	Asp	Asn	Gly	Asn	
				245					250					255		
cct	gcc	ctc	gac	tgc	cca	tac	cag	aag	gtc	ctg	gac	ggc	gtc	ctc	aac	816
Pro	Ala	Leu	Asp	Cys	Pro	Tyr	Gln	Lys	Val	Leu	Asp	Gly	Val	Leu	Asn	
			260					265					270			
tat	ccg	atc	tac	tgg	caa	ctc	ctc	tac	gcc	ttc	gaa	tcc	tcc	agc	ggc	864
Tyr	Pro	Ile	Tyr	Trp	Gln	Leu	Leu	Tyr	Ala	Phe	Glu	Ser	Ser	Ser	Gly	
		275						280					285			
agc	atc	agc	aac	ctc	tac	aac	atg	atc	aaa	tcc	gtc	gca	agc	gac	tgc	912
Ser	Ile	Ser	Asn	Leu	Tyr	Asn	Met	Ile	Lys	Ser	Val	Ala	Ser	Asp	Cys	
		290				295					300					
tcc	gat	ccg	aca	cta	ctc	ggc	aac	ttc	atc	gaa	aac	cac	gac	aat	ccc	960
Ser	Asp	Pro	Thr	Leu	Leu	Gly	Asn	Phe	Ile	Glu	Asn	His	Asp	Asn	Pro	
305					310					315					320	
cgt	ttc	gcc	tcc	tac	acc	tcc	gac	tac	tcg	caa	gcc	aaa	aac	gtc	ctc	1008
Arg	Phe	Ala	Ser	Tyr	Thr	Ser	Asp	Tyr	Ser	Gln	Ala	Lys	Asn	Val	Leu	
				325					330					335		
agc	tac	atc	ttc	ctc	tcc	gac	ggc	atc	ccc	atc	gtc	tac	gcc	ggc	gaa	1056
Ser	Tyr	Ile	Phe	Leu	Ser	Asp	Gly	Ile	Pro	Ile	Val	Tyr	Ala	Gly	Glu	
			340					345					350			
gaa	cag	cac	tac	tcc	ggc	ggc	aag	gtg	ccc	tac	aac	cgc	gaa	gcg	acc	1104
Glu	Gln	His	Tyr	Ser	Gly	Gly	Lys	Val	Pro	Tyr	Asn	Arg	Glu	Ala	Thr	
		355				360					365					
tgg	ctt	tca	ggc	tac	gac	acc	tcc	gca	gag	ctg	tac	acc	tgg	ata	gcc	1152
Trp	Leu	Ser	Gly	Tyr	Asp	Thr	Ser	Ala	Glu	Leu	Tyr	Thr	Trp	Ile	Ala	
		370				375					380					
acc	acg	aac	gcg	atc	cgc	aaa	cta	gcc	atc	tca	gct	gac	tcg	gcc	tac	1200
Thr	Thr	Asn	Ala	Ile	Arg	Lys	Leu	Ala	Ile	Ser	Ala	Asp	Ser	Ala	Tyr	
385					390					395					400	
att	acc	tac	gcg	aat	gat	gca	ttc	tac	act	gac	agc	aac	acc	atc	gca	1248
Ile	Thr	Tyr	Ala	Asn	Asp	Ala	Phe	Tyr	Thr	Asp	Ser	Asn	Thr	Ile	Ala	
				405					410					415		
atg	cgc	aaa	ggc	acc	tca	ggg	agc	caa	gtc	atc	acc	gtc	ctc	tcc	aac	1296
Met	Arg	Lys	Gly	Thr	Ser	Gly	Ser	Gln	Val	Ile	Thr	Val	Leu	Ser	Asn	
			420					425					430			
aaa	ggc	tcc	tca	gga	agc	agc	tac	acc	ctg	acc	ctc	agc	gga	agc	ggc	1344
Lys	Gly	Ser	Ser	Gly	Ser	Ser	Tyr	Thr	Leu	Thr	Leu	Ser	Gly	Ser	Gly	
		435						440				445				
tac	aca	tcc	ggc	acg	aag	ctg	atc	gaa	gcg	tac	aca	tgc	aca	tcc	gtg	1392
Tyr	Thr	Ser	Gly	Thr	Lys	Leu	Ile	Glu	Ala	Tyr	Thr	Cys	Thr	Ser	Val	
		450				455					460					
acc	gtg	gac	tcg	agc	ggc	gat	att	ccc	gtg	ccg	atg	gcg	tcg	gga	tta	1440
Thr	Val	Asp	Ser	Ser	Gly	Asp	Ile	Pro	Val	Pro	Met	Ala	Ser	Gly	Leu	
465					470				475						480	
ccg	aga	gtt	ctt	ctg	ccc	gcg	tcc	gtc	gtc	gat	agc	tct	tcg	ctc	tgt	1488
Pro	Arg	Val	Leu	Leu	Pro	Ala	Ser	Val	Val	Asp	Ser	Ser	Ser	Leu	Cys	
				485					490					495		
ggc	ggg	agc	gga	aga	tta	tac	gtc	gag	taa							1518

Gly Gly Ser Gly Arg Leu Tyr Val Glu
500 505

<210> 17

<211> 505

<212> PRT

<213> Aspergillus niger

<400> 17

Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly
1 5 10 15
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
20 25 30
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
35 40 45
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
50 55 60
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65 70 75 80
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
85 90 95
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
100 105 110
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
115 120 125
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
130 135 140
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
145 150 155 160
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
165 170 175
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
180 185 190
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
195 200 205
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
210 215 220
Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
225 230 235 240
Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
245 250 255
Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
260 265 270
Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
275 280 285
Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
290 295 300
Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
305 310 315 320
Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
325 330 335
Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
340 345 350
Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
355 360 365
Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala

370		375		380
Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr				
385		390		395
				400

Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala				
	405		410	415
Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn				
	420		425	430
Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly				
	435		440	445
Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val				
	450		455	460
Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu				
	465		470	475
Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys				
	485		490	495
Gly Gly Ser Gly Arg Leu Tyr Val Glu				
	500		505	

<210> 18
 <211> 2935
 <212> DNA
 <213> *Penicillium chrysogenum*

<400> 18

ggttcgaaga	ggccaagata	ttatatcgag	gagtagagca	aaaataatgc	tgatatatta	60
atgaagagat	gacaattccg	acttccaact	tccaacttgg	acctcggagt	tggtgaatcc	120
ggtcctgctt	gccccatata	gcttccgacc	accggatttg	gaccaatcaa	cgcaggaaga	180
tgtcagcagc	ttcaggcatc	agcgtcacct	gaccttcgtg	ttgcccgcgt	caacgagcgc	240
gtctcaatga	tacttttagac	ttgattaatt	tacacctttt	aatatttcca	atctcccag	300
gatacctact	tcgtaacaat	ggttgaagat	agctacacgc	gcgaggagga	gaattacgag	360
gatgaagagc	tcgacgagac	cgtgagtatc	aaaagttgga	gatatagtta	ccgattggtg	420
acggttgcct	acatagagct	tcaaatcagt	caaagatgcg	gtgctgtttg	ctatagatat	480
tagcagttcg	atgctcacgc	ctcgtccatc	gcctgatcct	aagaaacatg	gagacgaatc	540
acccgcgtct	gcagctttga	agtgtgcata	ccatctgatg	caacaacgca	tcattctcaa	600
ccctcatgac	atgattggcg	ttttgcttta	cggaaacgca	tcttccaagt	tctatgatga	660
aaatgaggat	gaccgtggag	atctctcata	tcctcactgt	tatctgtaca	cggatcttga	720
tgttccatca	gcccaggaag	tcaagcaact	gcggtccctc	gcattctccag	cagatgctga	780
tgatgacgta	ctgcaagttt	tggagccatc	aaaggagcca	gcctccatgg	ccaacatgct	840
tttctgcgcc	aaccaaactc	ttacctcaaa	agctccaaac	tttgcttctc	gacgcctggt	900
tgctgtgacc	gacaacgata	atccccacgc	agacaacaaa	ggaatgcggt	ctgctgcaac	960
agttcgtgcg	agggacttgt	acgatcttgg	tgtaaatatc	gagttgtttc	ccatatctca	1020
accagaccac	gaattcgaca	cctctaaatt	ctacgacgta	ggtcattaac	cttgattgca	1080
taggggtata	ctcacaattg	gcaggacatt	atctacaaaa	catcgcccag	tgatggagat	1140
gcccctgcat	acctacagcc	ggataccaac	acatcaacag	ctaaaggcga	tggaactttca	1200
ttgctcaatt	ctctgttgtc	gagcatcaac	tcacgatctg	tccccgcg	atcgctgttc	1260
tcaaatgtgc	cacttgagat	cggacctaat	ttcaaaaatat	ccgtcaatgg	atatttgctt	1320
ctcaagaaac	aagagcctgc	aaggagtgtc	ttcgtctggc	aaggaggcga	gactgctcag	1380
attgccaag	gagtcacaac	tctaattgtc	gatgacacag	ggcaggagat	tgagaagtct	1440
gacattcgca	aggcatacaa	gtttggtggc	gagcaggtat	cattcaccat	cgaagaacaa	1500
caggcgctaa	gaagcttcgg	tgacccgggtg	atccgtatta	ttgggttcaa	gccactgtca	1560
gccctccggt	tctgggcca	tgtcaagcac	ccctcgttta	tttatccctc	tgaagaggac	1620
tacgtcgggt	caacaagagt	cttttctgca	ctgcattcga	aactcctcga	atcgagagaa	1680


```

ctggctttgg tctggttcat ccccgcgaga aatgcctcac cagtcttagc tgctatgatt 1740
gcagggtgctg agaagatcga cgagaatggc gtgcagaaaa ttccacctgg gatgtggatt 1800
atccctcttc ctttcgcaga tgatgtgcgc caaaatccag agagcaccgt ccaccgggca 1860
ggagatgcgc tgaacgacgc catgcgagat gttgttcgcc agttgcagct ccccaaggct 1920
gtgtacgate cttcaaaata tccgaatcct tgtgagcctt cgtcacttca atctttggga 1980
caatgatact gactgattcg cagcgcttca atggcattat cgtatcttac aggctatcgc 2040
cttggatgaa gatttcccag aatcaccaga tgacaagacc gtgcctaagt accgacagg 2100
tcacaagggt ggctgcttcc atgatcccag aaatgcccga acgtactgac caaatggatg 2160
ttctagcgcg ctggcgacta tattcttaga tgggcccagg aactgaaatt gcaagcctcc 2220
gagatgtttg gtgggtcagt agccgccacc tctacgctgg taaagcgagg tgccaagacc 2280
gaggcagctg gtgagcacc atcaaagcgg gtgaagggtg aagacagtga gcccgaggatg 2340
gaagacgaag tgaagaaatg ctatgcgaaa ggcactgttt ccaagggtgag cattcaaatt 2400
ctcccagggt attgaccaa ctaatactcg ccttcagctt acggtggccg tgctgaagga 2460
attcttgcat gcacatggcc gtgctacagc aggaaagaaa gcagatctcg tggaccgagt 2520
tgagcagtac tttgagcaga agttttaaac attgatttga agtttgctca ggatcgtctt 2580
gggggtggtcc aagggttgctg taatctgcgg cccgtttaat gagttatgag tgtatcctac 2640
ttgctgttt ccataagggtc atagtcattt caaatgaatc gatatctttt atccaggatg 2700
atgttaggga cattatatat aagaatatac cggcgtttct ttttcgatgt cttttcagat 2760
gtatacaaag gcgcaagccg gtaaaaggcg tgaacgcct gatatatatc accgatactt 2820
ctttatgcaa aatgccagaa aatacctcta gcaactacag gggtagaaaa agagatcacc 2880
cttccaagggt tggcctagtc ttcctagata gccttctccg atagtcactt catac 2935

```

<210> 19

<211> 1977

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (1977)

<400> 19

```

atg gtt gaa gat agc tac acg cgc gag gag gag aat tac gag gat gaa 48
Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Glu Asn Tyr Glu Asp Glu
1 5 10 15
gag ctc gac gag acc agc ttc aaa tca gtc aaa gat gcg gtg ctg ttt 96
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe
20 25 30
gct ata gat att agc agt tcg atg ctc acg cct cgt cca tcg cct gat 144
Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
35 40 45
cct aag aaa cat gga gac gaa tca ccc gcg tct gca gct ttg aag tgt 192
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
50 55 60
gca tac cat ctg atg caa caa cgc atc atc tcc aac cct cat gac atg 240
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65 70 75 80
att ggc gtt ttg ctt tac gga acg caa tct tcc aag ttc tat gat gaa 288
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
85 90 95
aat gag gat gac cgt gga gat ctc tca tat cct cac tgt tat ctg tac 336
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
100 105 110
acg gat ctt gat gtt cca tca gcc cag gaa gtc aag caa ctg cgg tcc 384
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
115 120 125

```

ctc gca tct cca gca gat gct gat gat gac gta ctg caa gtt ttg gag	432
Leu Ala Ser Pro Ala Asp Ala Asp Asp Asp Val Leu Gln Val Leu Glu	
130 135 140	
cca tca aag gag cca gcc tcc atg gcc aac atg ctt ttc tgc gcc aac	480
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn	
145 150 155 160	
caa atc ttt acc tca aaa gct cca aac ttt gct tct cga cgc ctg ttt	528
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe	
165 170 175	
gtc gtg acc gac aac gat aat ccc cac gca gac aac aaa gga atg cgg	576
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg	
180 185 190	
tct gct gca aca gtt cgt gcg agg gac ttg tac gat ctt ggt gtc aat	624
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn	
195 200 205	
atc gag ttg ttt ccc ata tct caa cca gac cac gaa ttc gac acc tct	672
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser	
210 215 220	
aaa ttc tac gac gac att atc tac aaa aca tcg ccc agt gat gga gat	720
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp	
225 230 235 240	
gcc cct gca tac cta cag ccg gat acc aac aca tca aca gct aaa ggc	768
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly	
245 250 255	
gat gga ctt tca ttg ctc aat tct ctg ttg tcg agc atc aac tca cga	816
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg	
260 265 270	
tct gtc ccc cgc cga tcg ctg ttc tca aat gtg cca ctt gag atc gga	864
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly	
275 280 285	
cct aat ttc aaa ata tcc gtc aat gga tat ttg ctt ctc aag aaa caa	912
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Leu Lys Lys Gln	
290 295 300	
gag cct gca agg agt tgc ttc gtc tgg caa gga ggc gag act gct cag	960
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln	
305 310 315 320	
att gcc aaa gga gtc aca act cta atg tct gat gac aca ggg cag gag	1008
Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu	
325 330 335	
att gag aag tct gac att cgc aag gca tac aag ttt ggt ggc gag cag	1056
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln	
340 345 350	
gta tca ttc acc atc gaa gaa caa cag gcg cta aga agc ttc ggt gac	1104
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp	
355 360 365	
ccg gtg atc cgt att att ggg ttc aag cca ctg tca gcc ctc ccg ttc	1152
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe	
370 375 380	
tgg gcc aat gtc aag cac ccc tcg ttt att tat ccc tct gaa gag gac	1200
Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp	
385 390 395 400	
tac gtc ggt tca aca aga gtc ttt tct gca ctg cat cag aaa ctc ctc	1248
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu	
405 410 415	
gaa tcg gag aaa ctg gct ttg gtc tgg ttc atc ccc cgc aga aat gcc	1296
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala	
420 425 430	

tca cca gtc tta gct gct atg att gca ggt gct gag aag atc gac gag	1344
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu	
435 440 445	
aat ggc gtg cag aaa att cca cct ggg atg tgg att atc cct ctt cct	1392
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro	
450 455 460	
ttc gca gat gat gtg cgc caa aat cca gag agc acc gtc cac cgg gca	1440
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala	
465 470 475 480	
gga gat gcg ctg aac gac gcc atg cga gat gtt gtt cgc cag ttg cag	1488
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln	
485 490 495	
ctc ccc aag gct gtg tac gat cct tca aaa tat ccg aat cct tcg ctt	1536
Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu	
500 505 510	
caa tgg cat tat cgt atc tta cag gct atc gcc ttg gat gaa gat ttc	1584
Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe	
515 520 525	
cca gaa tca cca gat gac aag acc gtg cct aag tac cga cag gtt cac	1632
Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His	
530 535 540	
aag gtt ggc tgc ttc cat gat ccc aga aat gcc cga aca tgg gcc gag	1680
Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu	
545 550 555 560	
gaa ctg aaa ttg caa gcc tcc gag atg ttt ggt ggg tca gta gcc gcc	1728
Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala	
565 570 575	
acc tct acg ctg gta aag cga ggt gcc aag acc gag gca gct ggt gag	1776
Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu	
580 585 590	
cac cca tca aag cgg gtg aag gtt gaa gac agt gag ccc gga gtg gaa	1824
His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu	
595 600 605	
gac gaa gtg aag aaa tgc tat gcg aaa ggc act gtt tcc aag ctt acg	1872
Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr	
610 615 620	
gtg gcc gtg ctg aag gaa ttc ttg cat gca cat ggc cgt gct aca gca	1920
Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala	
625 630 635 640	
gga aag aaa gca gat ctc gtg gac cga gtt gag cag tac ttt gag cag	1968
Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln	
645 650 655	
aag ttt taa	1977
Lys Phe	

<210> 20

<211> 658

<212> PRT

<213> Penicillium chrysogenum

<400> 20

Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Glu Asn Tyr Glu Asp Glu	
1 5 10 15	
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe	
20 25 30	

Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
 35 40 45
 Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
 50 55 60
 Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
 65 70 75 80
 Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
 85 90 95
 Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
 100 105 110
 Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
 115 120 125
 Leu Ala Ser Pro Ala Asp Ala Asp Asp Val Leu Gln Val Leu Glu
 130 135 140
 Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
 145 150 155 160
 Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
 165 170 175
 Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg
 180 185 190
 Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
 195 200 205
 Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser
 210 215 220
 Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
 225 230 235 240
 Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly
 245 250 255
 Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg
 260 265 270
 Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
 275 280 285
 Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Lys Lys Gln
 290 295 300
 Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln
 305 310 315 320
 Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu
 325 330 335
 Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln
 340 345 350
 Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp
 355 360 365
 Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe
 370 375 380
 Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp
 385 390 395 400
 Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu
 405 410 415
 Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala
 420 425 430
 Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
 435 440 445
 Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
 450 455 460
 Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala
 465 470 475 480
 Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln

				485						490						495			
Leu	Pro	Lys	Ala	Val	Tyr	Asp	Pro	Ser	Lys	Tyr	Pro	Asn	Pro	Ser	Leu				
			500					505					510						
Gln	Trp	His	Tyr	Arg	Ile	Leu	Gln	Ala	Ile	Ala	Leu	Asp	Glu	Asp	Phe				
		515					520					525							
Pro	Glu	Ser	Pro	Asp	Asp	Lys	Thr	Val	Pro	Lys	Tyr	Arg	Gln	Val	His				
	530					535					540								
Lys	Val	Gly	Cys	Phe	His	Asp	Pro	Arg	Asn	Ala	Arg	Thr	Trp	Ala	Glu				
545					550				555						560				
Glu	Leu	Lys	Leu	Gln	Ala	Ser	Glu	Met	Phe	Gly	Gly	Ser	Val	Ala	Ala				
				565					570					575					
Thr	Ser	Thr	Leu	Val	Lys	Arg	Gly	Ala	Lys	Thr	Glu	Ala	Ala	Gly	Glu				
			580					585					590						
His	Pro	Ser	Lys	Arg	Val	Lys	Val	Glu	Asp	Ser	Glu	Pro	Gly	Val	Glu				
	595					600					605								
Asp	Glu	Val	Lys	Lys	Cys	Tyr	Ala	Lys	Gly	Thr	Val	Ser	Lys	Leu	Thr				
	610				615				620										
Val	Ala	Val	Leu	Lys	Glu	Phe	Leu	His	Ala	His	Gly	Arg	Ala	Thr	Ala				
625				630				635						640					
Gly	Lys	Lys	Ala	Asp	Leu	Val	Asp	Arg	Val	Glu	Gln	Tyr	Phe	Glu	Gln				
			645				650						655						

Lys Phe

<210> 21

<211> 3605

<212> DNA

<213> *Penicillium chrysogenum*

<400> 21

gatttcggat	atgttatgac	ctaaggagag	ttgagttggc	gataaagtcg	atgtgaagtt	60
gcacgcaggg	gaagaagtgg	cagttatcgc	tacgatccaa	ttcttaataa	aagc cttatt	120
tccacttcca	aataagaggga	gctggcttct	aacgacgcac	agaccaccaa	acac caacaa	180
agacggcgtg	tgatgtcatg	tgccttcgtg	tttcgggtcta	aaccgcaagt	ggaa atatca	240
cgcgtctgcc	tggtgtcttg	agccccaaag	caactttgtc	ttgccatttt	ccca acatca	300
tcatcattat	ggcggagaaa	gaggctacag	tttacattgt	agacatggga	cggg ctatgg	360
gcgagcgcca	ccatggccgt	cctatgacag	atctcgaatg	ggccatgcag	tatgtctggg	420
ataggatcac	tgccacggta	tgtgacttga	ccttgttcaa	cgccagagaa	ctga caattc	480
caggtggcta	ctggtcgaaa	gacggctacg	gttggcgtag	ttggactcag	gact gatggg	540
gagtggtcgg	ctaccagtca	gcacccattg	ggacccttgt	ctcatgtttg	gaac aggaac	600
tatcaacgac	ttggaagaag	agagcttttc	taatatttct	attctcttcg	gtct tggcca	660
gtatgtgtgg	cttaattaat	cgacagcttt	atgccgagtc	gcctgactaa	attgtctttc	720
agagtctcca	tgctgatgat	cgggaaactg	cgagaaacga	tcaagcccag	caac actaac	780
agaggcgatg	gtatgtgact	gttgaagtct	tgtcaagctg	cttattctga	cttt atataa	840
gccatctctt	ctattgtcat	tgccatgcag	atgatcattg	actacacgaa	gaaa aacaaa	900
tacaagcgca	agatcatctt	ggtgaccaat	ggtaccggcg	tgatgagcga	tgat aatata	960
gaaggcatca	ttgaaaagat	gaaagagggt	aacattgagt	tggtgggtcat	gtat gtttct	1020
tgccgacatg	acttcacatt	catgctaata	ctatgcagtg	gagccgattt	tgat gacgct	1080
gagtatgggt	ttaaaggaaga	agacaaagac	agtcgaaagg	ttctaagcca	tctc caatct	1140
attctgttat	tcatgttgac	aaagcgcctc	gcaggctgaa	aacgagactt	ttct ccgaag	1200
cctggctgag	gactgcgaag	gtgcttatgg	aacgctggag	caagccgttt	cgga attgga	1260
tattccccgt	atcaaagtga	ccaagagcat	gccatcttct	aagggaaacc	tcac gctcgg	1320
caatccccgag	gagtatgaca	cggctatgac	tatacccggt	gagcgatact	tcgaaaccta	1380
cgtcgccaaa	ccaatctcag	cgagctcggt	cgtaccacgc	tccggcaccg	aacc tggaag	1440
tcaagcaccg	gttaaaggcg	atgctgaagg	cgatgctctc	gcctcagtg	gaac atcacg	1500
gacgtatcag	atcacagatg	agtcgcgacc	aggtggtaag	atcgacgttg	aacg cgatga	1560
cctcgccaag	gggtacgagt	acggacgtac	cgcgggttct	atcgagcaaa	ccga tgagaa	1620

tgttgcaaat	ctacaaacat	ttgctggtat	ggggctgac	gggttcgttc	agaaggatca	1680
gggtgtgtctt	tatgcccaata	ttaagtgtta	taacagctaa	tccgtgactt	agtatgaccg	1740
gtacatgcat	atgtcaaaca	cgaatatcat	catccctcag	cgtgcaaatg	actatgcgtc	1800
tcttgcggtt	tcttctctca	ttcatgcact	ctacgaattg	gagtcctatg	cgggttgcctg	1860
cttggtgacc	aaagaatcca	aaccaccgat	gcttgtgttg	ctagctccat	ctatcgagggc	1920
agactatgag	tgcttgattg	aagtacagct	tccatttgca	gaagacgtgc	ggtcgtatcg	1980
gttccacact	ttggataaga	ttatcactgt	ctctggcaag	gtggtgactg	aacatcgaaa	2040
cctcccaagc	gtggcggtga	aagatgcgat	gagtaactac	gtggacagca	tggattttgt	2100
caccacaaac	gacgaagggt	aagtatagtc	tacttgatta	tgcactttat	cagttaatca	2160
aaagagccag	gcaagccact	gacgatctcc	caatcgacga	gtcattctca	cggttattgc	2220
accgcacgca	atcagcagtt	cgatatcggt	ctgtgcatcc	caatgaccct	gtcctcgacc	2280
cctcagagcg	gctcactgaa	ttcgacacac	cctcagaaga	catggtcaag	aactccaaat	2340
cccattctga	gaaattgatg	tccatagcag	atgtcaagaa	aggtaacctc	gatttccata	2400
ctacatccgg	aagataccct	actcaccac	gcattttgtc	ttatagttcc	accgaagaca	2460
aaaggccgta	aacgccaacg	tgaaacagag	aaacctctct	caggtttgga	cgtggacgcc	2520
ctgctcagcc	tgaacccaa	gcgaacgaag	atttccaccg	agaatgcaat	cccagagttc	2580
aagcaaacac	tttcccgcgc	ggaaaacatc	gacgcaatcc	acgacgctgt	gcagcagatg	2640
gctaaaatca	tgcagagcca	gatcacacac	agcctcggtc	attcaaatta	cgaccgtgtt	2700
atcgaggggc	ttggtactat	gcgtgaagaa	ctggtggact	atgaggaacc	ggcgggtgtac	2760
aatgactttg	tgcgtcagtt	gaagggcaag	atgttgcggt	aggagctggg	tggggatcgg	2820
agggagctgt	ggtgggtttgt	aaggaaggga	aagcttgggc	tcattggcaa	gagtgaaggtg	2880
gatagctcgg	ctgttgagga	gcaagaggct	caagagggtga	ggtttggcct	tttattgtgg	2940
aatggaacga	gtgctaacac	tgcgtatagt	ttctggctcc	caattgagga	attgagtggtg	3000
ggggcggtgt	attgtctcgc	tattcaaaca	tgaaatagt	agcatagcag	ggatgtggaa	3060
tattcatact	attctctatg	ccagatttac	gcgatgtaga	gcttctctgt	gaagttatgt	3120
tatatggtac	gtcgtagaag	taaggccggg	aaacggagta	tagtccacct	cagggtgatga	3180
ggtccaataa	tactgaccac	ccagatcaaa	ggatagcgat	tggaggggtt	acggagaaat	3240
ggaaatattg	agcaagccca	tgaacagcat	tgtcatatag	acgtagaatt	gacacataca	3300
ggaacgaagc	ccgcagacag	aacaatatga	ggcacgaagt	gaatcggtgc	ccaattgcaa	3360
ggcatgacga	gtcgtcaatg	aacaacagaa	ccaaacgccg	tgcataacat	gcccataaac	3420
cagtattcgc	tccagaaaaa	agcaaaagac	cgagatttgc	aaactcaaac	attaaaaagc	3480
atccagatgc	atcagggaaa	aggggtatgc	agaagtgttg	tcccggtagg	acgagaagaa	3540
tggaacaaga	agcgctccga	ggaaacttgg	agagtttcga	ggggcgaaaag	aagagagcag	3600
aacat						3605

<210> 22

<211> 2157

<212> DNA

<213> Penicillium chrysogenum

<220>

<221> CDS

<222> (1)..(2157)

<400> 22

atg	gcg	gag	aaa	gag	gct	aca	gtt	tac	att	gta	gac	atg	gga	cgg	tct	48
Met	Ala	Glu	Lys	Glu	Ala	Thr	Val	Tyr	Ile	Val	Asp	Met	Gly	Arg	Ser	
1			5					10						15		
atg	ggc	gag	cgc	cac	cat	ggc	cgt	cct	atg	aca	gat	ctc	gaa	tgg	gcc	96
Met	Gly	Glu	Arg	His	His	Gly	Arg	Pro	Met	Thr	Asp	Leu	Glu	Trp	Ala	
			20					25					30			
atg	cag	tat	gtc	tgg	gat	agg	atc	act	gcc	acg	gtg	gct	act	ggt	cga	144
Met	Gln	Tyr	Val	Trp	Asp	Arg	Ile	Thr	Ala	Thr	Val	Ala	Thr	Gly	Arg	
			35				40					45				
aag	acg	gct	acg	gtt	ggc	gta	gtt	gga	ctc	agg	act	gat	gtc	agc	acc	192
Lys	Thr	Ala	Thr	Val	Gly	Val	Val	Gly	Leu	Arg	Thr	Asp	Val	Ser	Thr	

50	cat	tg	gac	cct	tgt	ctc	atg	ttt	gga	aca	gga	act	atc	aac	gac	ttg	240
	His	Trp	Asp	Pro	Cys	Leu	Met	Phe	Gly	Thr	Gly	Thr	Ile	Asn	Asp	Leu	
65						70										80	
	gaa	gaa	gag	agc	ttt	tct	aat	att	tct	att	ctc	ttc	ggg	ctt	ggc	caa	288
	Glu	Glu	Glu	Ser	Phe	Ser	Asn	Ile	Ser	Ile	Leu	Phe	Gly	Leu	Gly	Gln	
					85				90					95			
	gtc	ctc	atg	cct	gat	atc	cgg	aaa	ctg	cga	gaa	acg	atc	aag	ccc	agc	336
	Val	Leu	Met	Pro	Asp	Ile	Arg	Lys	Leu	Arg	Glu	Thr	Ile	Lys	Pro	Ser	
				100					105					110			
	aac	act	aac	aga	ggc	gat	gcc	atc	tct	tct	att	gtc	att	gcc	atg	cag	384
	Asn	Thr	Asn	Arg	Gly	Asp	Ala	Ile	Ser	Ser	Ile	Val	Ile	Ala	Met	Gln	
				115				120					125				
	atg	atc	att	gac	tac	acg	aag	aaa	aac	aaa	tac	aag	cgc	aag	atc	atc	432
	Met	Ile	Ile	Asp	Tyr	Thr	Lys	Lys	Asn	Lys	Tyr	Lys	Arg	Lys	Ile	Ile	
				130				135					140				
	ttg	gtg	acc	aat	ggg	acc	ggc	gtg	atg	agc	gat	gat	aat	atc	gaa	ggc	480
	Leu	Val	Thr	Asn	Gly	Thr	Gly	Val	Met	Ser	Asp	Asp	Asn	Ile	Glu	Gly	
	145					150					155					160	
	atc	att	gaa	aag	atg	aaa	gag	gtt	aac	att	gag	ttg	gtg	gtc	atg	tat	528
	Ile	Ile	Glu	Lys	Met	Lys	Glu	Val	Asn	Ile	Glu	Leu	Val	Val	Met	Tyr	
					165						170				175		
	tat	ggg	gta	aag	gaa	gaa	gac	aaa	gac	agt	cga	aag	gct	gaa	aac	gag	576
	Tyr	Gly	Val	Lys	Glu	Glu	Asp	Lys	Asp	Ser	Arg	Lys	Ala	Glu	Asn	Glu	
				180				185					190				
	act	ttt	ctc	cga	agc	ctg	gct	gag	gac	tgc	gaa	ggg	gct	tat	gga	acg	624
	Thr	Phe	Leu	Arg	Ser	Leu	Ala	Glu	Asp	Cys	Glu	Gly	Ala	Tyr	Gly	Thr	
				195				200					205				
	ctg	gag	caa	gcc	gtt	tcg	gaa	ttg	gat	att	ccc	cgt	atc	aaa	gtg	acc	672
	Leu	Glu	Gln	Ala	Val	Ser	Glu	Leu	Asp	Ile	Pro	Arg	Ile	Lys	Val	Thr	
				210				215					220				
	aag	agc	atg	cca	tct	ttc	aag	gga	aac	ctc	acg	ctc	ggc	aat	ccc	gag	720
	Lys	Ser	Met	Pro	Ser	Phe	Lys	Gly	Asn	Leu	Thr	Leu	Gly	Asn	Pro	Glu	
	225					230					235					240	
	gag	tat	gac	acg	gct	atg	act	ata	ccc	gtg	gag	cga	tac	ttc	cga	acc	768
	Glu	Tyr	Asp	Thr	Ala	Met	Thr	Ile	Pro	Val	Glu	Arg	Tyr	Phe	Arg	Thr	
					245					250					255		
	tac	gtc	gcc	aaa	cca	atc	tca	gcg	agc	tcg	ttc	gta	cca	cgc	tcc	ggc	816
	Tyr	Val	Ala	Lys	Pro	Ile	Ser	Ala	Ser	Ser	Phe	Val	Pro	Arg	Ser	Gly	
				260				265							270		
	acc	gaa	cct	gga	agt	caa	gca	ccg	gtt	aaa	ggc	gat	gct	gaa	ggc	gat	864
	Thr	Glu	Pro	Gly	Ser	Gln	Ala	Pro	Val	Lys	Gly	Asp	Ala	Glu	Gly	Asp	
				275				280					285				
	gct	ctc	gcc	tca	gtg	cga	aca	tca	cgg	acg	tat	cag	atc	aca	gat	gag	912
	Ala	Leu	Ala	Ser	Val	Arg	Thr	Ser	Arg	Thr	Tyr	Gln	Ile	Thr	Asp	Glu	
				290				295					300				
	tcc	gca	cca	ggg	ggg	aag	atc	gac	gtt	gaa	cgc	gat	gac	ctc	gcc	aag	960
	Ser	Ala	Pro	Gly	Gly	Lys	Ile	Asp	Val	Glu	Arg	Asp	Asp	Leu	Ala	Lys	
	305					310					315					320	
	ggg	tac	gag	tac	gga	cgt	acc	gcg	gtt	cct	atc	gag	caa	acc	gat	gag	1008
	Gly	Tyr	Glu	Tyr	Gly	Arg	Thr	Ala	Val	Pro	Ile	Glu	Gln	Thr	Asp	Glu	
					325					330					335		
	aat	gtt	gca	aat	cta	caa	aca	ttt	gct	ggg	atg	ggg	ctg	atc	ggg	ttc	1056
	Asn	Val	Ala	Asn	Leu	Gln	Thr	Phe	Ala	Gly	Met	Gly	Leu	Ile	Gly	Phe	
				340				345							350		
	gtt	cag	aag	gat	cag	tat	gac	cgg	tac	atg	cat	atg	tca	aac	acg	aat	1104
	Val	Gln	Lys	Asp	Gln	Tyr	Asp	Arg	Tyr	Met	His	Met	Ser	Asn	Thr	Asn	

atc	atc	atc	cct	cag	cgt	gca	aat	gac	tat	gcg	tct	ctt	gcg	ttg	tct	1152
Ile	Ile	Ile	Pro	Gln	Arg	Ala	Asn	Asp	Tyr	Ala	Ser	Leu	Ala	Leu	Ser	
	370					375					380					1200
tct	ctc	att	cat	gca	ctc	tac	gaa	ttg	gag	tcc	tat	gcg	gtt	gcc	cgc	
Ser	Leu	Ile	His	Ala	Leu	Tyr	Glu	Leu	Glu	Ser	Tyr	Ala	Val	Ala	Arg	
	385				390				395					400		1248
ttg	gtg	acc	aaa	gaa	tcc	aaa	cca	ccg	atg	ctt	gtg	ttg	cta	gct	cca	
Leu	Val	Thr	Lys	Glu	Ser	Lys	Pro	Pro	Met	Leu	Val	Leu	Leu	Ala	Pro	
			405						410					415		1296
tct	atc	gag	gca	gac	tat	gag	tgc	ttg	att	gaa	gta	cag	ctt	cca	ctt	
Ser	Ile	Glu	Ala	Asp	Tyr	Glu	Cys	Leu	Ile	Glu	Val	Gln	Leu	Pro	Phe	
			420					425					430			1344
gca	gaa	gac	gtg	cgg	tcg	tat	cgg	ttc	cca	cct	ttg	gat	aag	att	atc	
Ala	Glu	Asp	Val	Arg	Ser	Tyr	Arg	Phe	Pro	Pro	Leu	Asp	Lys	Ile	Ile	
			435				440						445			1392
act	gtc	tct	ggc	aag	gtg	gtg	act	gaa	cat	cga	aac	ctc	cca	agc	gtg	
Thr	Val	Ser	Gly	Lys	Val	Val	Thr	Glu	His	Arg	Asn	Leu	Pro	Ser	Val	
			450			455					460					1440
gcg	ttg	aaa	gat	gcg	atg	agt	aac	tac	gtg	gac	agc	atg	gat	ttt	gtc	
Ala	Leu	Lys	Asp	Ala	Met	Ser	Asn	Tyr	Val	Asp	Ser	Met	Asp	Phe	Val	
			465			470				475				480		1488
acc	aca	aac	gac	gaa	ggg	caa	gcc	act	gac	gat	ctc	cca	atc	gac	gag	
Thr	Thr	Asn	Asp	Glu	Gly	Gln	Ala	Thr	Asp	Asp	Leu	Pro	Ile	Asp	Glu	
			485						490					495		1536
tca	ttc	tca	ccg	tta	ttg	cac	cgc	atc	gaa	tca	gca	gtt	cga	tat	cgt	
Ser	Phe	Ser	Pro	Leu	Leu	His	Arg	Ile	Glu	Ser	Ala	Val	Arg	Tyr	Arg	
			500					505						510		1584
gct	gtg	cat	ccc	aat	gac	cct	gtc	ctc	gac	ccc	tca	gag	cgg	ctc	act	
Ala	Val	His	Pro	Asn	Asp	Pro	Val	Leu	Asp	Pro	Ser	Glu	Arg	Leu	Thr	
			515				520						525			1632
gaa	ttc	gca	cac	ccc	tca	gaa	gac	atg	gtc	aag	aac	tcc	aaa	tcc	cat	
Glu	Phe	Ala	His	Pro	Ser	Glu	Asp	Met	Val	Lys	Asn	Ser	Lys	Ser	His	
			530			535					540					1680
ctt	gag	aaa	ttg	atg	tcc	ata	gca	gat	gtc	aag	aaa	gtt	cca	ccg	aag	
Leu	Glu	Lys	Leu	Met	Ser	Ile	Ala	Asp	Val	Lys	Lys	Val	Pro	Pro	Lys	
			545			550				555				560		1728
aca	aaa	ggc	cgt	aaa	cgc	caa	cgt	gaa	aca	gag	aaa	cct	ctc	tca	ggt	
Thr	Lys	Gly	Arg	Lys	Arg	Gln	Arg	Glu	Thr	Glu	Lys	Pro	Leu	Ser	Gly	
			565					570						575		1776
ttg	gac	gtg	gac	gcc	ctg	ctc	agc	ctc	gaa	ccc	aag	cga	acg	aag	att	
Leu	Asp	Val	Asp	Ala	Leu	Leu	Ser	Leu	Glu	Pro	Lys	Arg	Thr	Lys	Ile	
			580					585						590		1824
tcc	acc	gag	aat	gca	atc	cca	gag	ttc	aag	caa	aca	ctt	tcc	cgc	gag	
Ser	Thr	Glu	Asn	Ala	Ile	Pro	Glu	Phe	Lys	Gln	Thr	Leu	Ser	Arg	Ala	
			595				600							605		1872
gaa	aac	atc	gac	gca	atc	cac	gac	gct	gtg	cag	cag	atg	gct	aaa	atc	
Glu	Asn	Ile	Asp	Ala	Ile	His	Asp	Ala	Val	Gln	Gln	Met	Ala	Lys	Ile	
			610			615								620		1920
atc	gag	agc	cag	atc	aca	cac	agc	ctc	ggt	cat	tca	aat	tac	gac	cgt	
Ile	Glu	Ser	Gln	Ile	Thr	His	Ser	Leu	Gly	His	Ser	Asn	Tyr	Asp	Arg	
			625			630				635				640		1968
gtt	atc	gag	ggg	ctt	ggt	act	atg	cgt	gaa	gaa	ctg	gtg	gac	tat	gag	
Val	Ile	Glu	Gly	Leu	Gly	Thr	Met	Arg	Glu	Glu	Leu	Val	Asp	Tyr	Glu	
			645					650						655		2016
gaa	ccg	gag	gtg	tac	aat	gac	ttt	gtg	cgt	cag	ttg	aag	ggc	aag	atg	
Glu	Pro	Ala	Val	Tyr	Asn	Asp	Phe	Val	Arg	Gln	Leu	Lys	Gly	Lys	Met	

660	665	670	
ttg cgg gag gag ctg ggt ggg gat cgg agg gag ctg tgg tgg ttt gta			2064
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val			
675	680	685	
agg aag gga aag ctt ggg ctc att ggc aag agt gag gtg gat agc tcg			2112
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser			
690	695	700	
gct gtt gag gag caa gag gct caa gag ttt ctg gct ccc aat tga			2157
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn			
705	710	715	

<210> 23

<211> 718

<212> PRT

<213> Penicillium chrysogenum

<400> 23

Met Ala Glu Lys Glu Ala Thr Val Tyr Ile Val Asp Met Gly Arg Ser	
1 5 10 15	
Met Gly Glu Arg His His Gly Arg Pro Met Thr Asp Leu Glu Trp Ala	
20 25 30	
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg	
35 40 45	
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr	
50 55 60	
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu	
65 70 75 80	
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln	
85 90 95	
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser	
100 105 110	
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln	
115 120 125	
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile	
130 135 140	
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly	
145 150 155 160	
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr	
165 170 175	
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu	
180 185 190	
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr	
195 200 205	
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr	
210 215 220	
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu	
225 230 235 240	
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr	
245 250 255	
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly	
260 265 270	
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp	
275 280 285	
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu	
290 295 300	
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys	

305					310					315				320	
Gly	Tyr	Glu	Tyr	Gly	Arg	Thr	Ala	Val	Pro	Ile	Glu	Gln	Thr	Asp	Glu
				325					330					335	
Asn	Val	Ala	Asn	Leu	Gln	Thr	Phe	Ala	Gly	Met	Gly	Leu	Ile	Gly	Phe
			340					345					350		
Val	Gln	Lys	Asp	Gln	Tyr	Asp	Arg	Tyr	Met	His	Met	Ser	Asn	Thr	Asn
		355					360					365			
Ile	Ile	Ile	Pro	Gln	Arg	Ala	Asn	Asp	Tyr	Ala	Ser	Leu	Ala	Leu	Ser
	370					375					380				
Ser	Leu	Ile	His	Ala	Leu	Tyr	Glu	Leu	Glu	Ser	Tyr	Ala	Val	Ala	Arg
385					390					395					400
Leu	Val	Thr	Lys	Glu	Ser	Lys	Pro	Pro	Met	Leu	Val	Leu	Leu	Ala	Pro
				405					410					415	
Ser	Ile	Glu	Ala	Asp	Tyr	Glu	Cys	Leu	Ile	Glu	Val	Gln	Leu	Pro	Phe
			420					425					430		
Ala	Glu	Asp	Val	Arg	Ser	Tyr	Arg	Phe	Pro	Pro	Leu	Asp	Lys	Ile	Ile
		435					440					445			
Thr	Val	Ser	Gly	Lys	Val	Val	Thr	Glu	His	Arg	Asn	Leu	Pro	Ser	Val
	450					455					460				
Ala	Leu	Lys	Asp	Ala	Met	Ser	Asn	Tyr	Val	Asp	Ser	Met	Asp	Phe	Val
465					470					475					480
Thr	Thr	Asn	Asp	Glu	Gly	Gln	Ala	Thr	Asp	Asp	Leu	Pro	Ile	Asp	Glu
				485					490					495	
Ser	Phe	Ser	Pro	Leu	Leu	His	Arg	Ile	Glu	Ser	Ala	Val	Arg	Tyr	Arg
			500					505					510		
Ala	Val	His	Pro	Asn	Asp	Pro	Val	Leu	Asp	Pro	Ser	Glu	Arg	Leu	Thr
		515					520					525			
Glu	Phe	Ala	His	Pro	Ser	Glu	Asp	Met	Val	Lys	Asn	Ser	Lys	Ser	His
	530					535					540				
Leu	Glu	Lys	Leu	Met	Ser	Ile	Ala	Asp	Val	Lys	Lys	Val	Pro	Pro	Lys
545					550					555					560
Thr	Lys	Gly	Arg	Lys	Arg	Gln	Arg	Glu	Thr	Glu	Lys	Pro	Leu	Ser	Gly
				565					570					575	
Leu	Asp	Val	Asp	Ala	Leu	Leu	Ser	Leu	Glu	Pro	Lys	Arg	Thr	Lys	Ile
			580					585					590		
Ser	Thr	Glu	Asn	Ala	Ile	Pro	Glu	Phe	Lys	Gln	Thr	Leu	Ser	Arg	Ala
		595					600					605			
Glu	Asn	Ile	Asp	Ala	Ile	His	Asp	Ala	Val	Gln	Gln	Met	Ala	Lys	Ile
	610					615					620				
Ile	Glu	Ser	Gln	Ile	Thr	His	Ser	Leu	Gly	His	Ser	Asn	Tyr	Asp	Arg
625					630					635					640
Val	Ile	Glu	Gly	Leu	Gly	Thr	Met	Arg	Glu	Glu	Leu	Val	Asp	Tyr	Glu
				645					650					655	
Glu	Pro	Ala	Val	Tyr	Asn	Asp	Phe	Val	Arg	Gln	Leu	Lys	Gly	Lys	Met
			660					665					670		
Leu	Arg	Glu	Glu	Leu	Gly	Gly	Asp	Arg	Arg	Glu	Leu	Trp	Trp	Phe	Val
		675					680					685			
Arg	Lys	Gly	Lys	Leu	Gly	Leu	Ile	Gly	Lys	Ser	Glu	Val	Asp	Ser	Ser
	690					695					700				
Ala	Val	Glu	Glu	Gln	Glu	Ala	Gln	Glu	Phe	Leu	Ala	Pro	Asn		
705					710					715					